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protein - protein search, using sw model

on: June 10, 2004, 11:04:47 ; Search time 95 seconds
(without alignments)
585.914 Million cell updates/sec

le: US-09-934-289a-18

fect score: 1146

uence: 1 MEPPGDWGPFPWRSTPRDV.....ECQHQTWPNHMCCKKAKG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :

A_Geneseq29Jan04:*

1: Geneseq1980s:*

2: Geneseq1980s:*

3: Geneseq2000s:*

4: Geneseq2000s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

alt No.	Score	Query Match	Length	DB ID	Description
1	1146	100.0	197	3	AAY79205 Soluble h
2	1146	100.0	197	6	ABU60682 Human sol
3	1065	92.9	193	3	AAY79204 Soluble h
4	1065	92.9	193	6	ABU60675 Human sol
5	1060	92.5	277	3	AAY79207 Membrane-
6	1060	92.5	277	6	ABU60694 Human mem
7	1060	92.5	283	2	AAY05809 Human tum
8	1060	92.5	283	2	AAY69238 Herpesvir
9	1060	92.5	283	2	AAY06488 Human tum
10	1060	92.5	283	3	AAY94721 Human TR2
11	1060	92.5	283	3	AAY95348 Human PRO
12	1060	92.5	283	3	AAY93695 Amino aci
13	1060	92.5	283	6	ABU60681 Human mem
14	1060	92.5	283	6	ABU60681 Human mem
15	1060	92.5	283	6	ABU58631 Human can
16	1060	92.5	283	6	ABU40215 Human cob
17	1060	92.5	283	6	ADA43035 Human her
18	1057	92.2	283	6	AAW60045 Human TNF
19	1057	92.2	283	2	AAW87591 Human tum
20	1057	92.2	283	3	AAW94717 Human TR2
21	1054	92.0	283	2	AAW95031 Tumour ne
22	1053	91.9	186	3	AAY79206 Soluble h
23	1053	91.9	186	6	ABU60688 Human sol
24	1052	91.8	283	2	AAW12659 Human her
25	1052	91.8	283	2	AAY05797 Herpes vi

26	925	80.7	159	6	ABU60683 Human mat
27	844	73.6	155	6	ABU60676 Human mat
28	839	73.2	239	6	ABU60695 Human mat
29	838	73.1	148	6	ABU60689 Human mat
30	604.5	52.7	185	2	AAW60046 Human TNF
31	604.5	52.7	185	3	AAW94716 Human TR2
32	604.5	52.7	240	2	AAW05810 Human tum
33	393	34.3	136	2	AAW60047 Human TNF
34	393	34.3	136	3	AAW94719 Human TR2
35	377.5	32.9	134	2	AAW05811 Human tum
36	292	25.5	278	3	AAW95322 Pig costi
37	261	22.8	207	4	AAW66980 Stu-t2 pr
38	261	22.8	325	2	AAR27865 Rabbit fi
39	261	22.8	325	2	AAR85071 Shope fib
40	261	22.8	659	6	ABJ37103 Concatame
41	260	22.7	461	2	AAR72504 p75 Tumou
42	259.5	22.6	462	6	AER40141 Human cvl
43	259	22.6	154	6	ADA20590 Fragment
44	259	22.6	183	2	AAR77421 BamIP del
45	259	22.6	184	5	AAW48061 Human TNF

ALIGNMENTS

RESULT 1

AAW79205
ID AAY79205 standard; protein; 197 AA.

XX AC AAY79205;

XX XX

DT 19-JUN-2000 (first entry)

DE Soluble herpesvirus entry mediator-2 (SHVEM2).

KW SHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor;

KW tumour necrosis factor receptor; human; herpes simplex virus; infection;

KW cancer; inflammation; autoimmune disorder; therapy; diagnosis.

XX OS Homo sapiens.

XX XX

PH Key Location/Qualifiers

FT Peptide 1..38

FT Protein /note= "signal peptide"

FT Protein 39..197

FT Protein /note= "mature protein, also separately claimed in Claim

FT Domain 42..75

FT Domain /note= "cysteine-rich domain"

FT Domain 78..119

FT Modified-site /note= "cysteine-rich domain"

FT Domain /note= "N-glycosylated"

FT Domain 121..162

FT Modified-site /note= "cysteine-rich domain"

FT Modified-site 173

FT Modified-site /note= "N-glycosylated"

PN WO200014230-A1.

XX PD 16-MAR-2000.

XX PD 03-SEP-1999; 99WO-US020180.

XX PF 03-SEP-1998; 98US-00146950.

XX PR 29-JUN-1999; 99US-00342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX PA Busfield SJ;

XX PI WPI; 2000-256981/22.

XX DR N-PSDB; AAZ94195.

New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays.

Claim 8; Fig 3; 149pp; English.

This polypeptide, the mature portion of which is also claimed, is human soluble herpesvirus entry mediator-2 (SHVEM2), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVEM). The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94196). SHVEM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TNFR) superfamily. It is thought to play a role analogous to other soluble members of the TNFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 cDNA molecules (see AAZ94195-97) which encode soluble forms (see AAY79204-06), and 1 cDNA molecule (see AAZ94198) that encodes a 2nd membrane-bound form (see AAY79207), of mHVEM. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders

Sequence 197 AA;

Query Match 100.0%; Score 1146; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
61 YRVKEACGELTGTVCCEPPTGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCCEPPTGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQTNPWNHMCCKKAKG 197
181 HQTNPWNHMCCKKAKG 197

SULT 2
160682

ABU60682 standard; protein; 197 AA.

ABU60682;

06-MAY-2003 (first entry)

Human soluble Herpesvirus Entry Mediator-2 (SHVEM-2).

Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM; SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicemia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;

asthma; psoriasis; apoptotic disorder; rheumatoid arthritis; systemic lupus erythematosus; insulin-dependent diabetes mellitus; cytotoxic disorder; septic shock; cachexia; proliferative disorder; B-cell cancer.

XX Homo sapiens.
XX US2002132297-A1.
XX 19-SEP-2002.
XX 21-AUG-2001; 2001US-00934289.
XX 03-SEP-1998; 98US-00146950.
XX (MILL-) MILLENNIUM PHARM INC.
XX Busfield SU;
XX WPI; 2003-255106/25.
XX N-PSDB; ABX90565, ABX90566.
XX New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.
XX Claim 8; Fig 3; 79pp; English.

XX The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mHVEM2 (where HVEM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to the and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein

Sequence 197 AA;

Query Match 100.0%; Score 1146; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
Db 1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
QY 61 YRVKEACGELTGTVCCEPPTGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCCEPPTGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HQTNPWNHMCCKKAKG 197
Db 181 HQTNPWNHMCCKKAKG 197

ULT 3
79204

AA779204 standard; protein; 193 AA.

AA779204;

19-JUN-2000 (first entry)

Soluble herpesvirus entry mediator-1 (SHVEM1).

SHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor;
tumour necrosis factor receptor; human; herpes simplex virus; infection;
cancer; inflammation; autoimmune disorder; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..36
Protein /note= "signal peptide"
8 /note= "mature protein, also separately claimed in Claim
Domain 42..75
Domain /note= "cysteine-rich domain"
78..119
Modified-site /note= "cysteine-rich domain"
110
Domain /note= "N-glycosylated"
121..162
Modified-site /note= "cysteine-rich domain"
173
/note= "N-glycosylated"

WO200014230-A1.

16-MAR-2000.

03-SEP-1999; 99WO-US020180.

03-SEP-1998; 98US-00146950.

29-JUN-1999; 99US-00342767.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Busfield SJ;

WPI; 2000-256981/22.

N-PSDB; AAZ94195.

New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
either in the soluble or membrane bound form, is useful in screening
assays and detection assays.

Claim 8; Fig 1; 149pp; English.

This polypeptide, the mature portion of which is also claimed, is human
soluble herpesvirus entry mediator-1 (SHVEM1), a novel soluble form of
membrane-bound herpesvirus entry mediator (mHVEM). The amino acid
sequence was deduced from an isolated cDNA clone (see AAZ94195). SHVEM1
is a TANGO-69-receptor and member of the tumour necrosis factor receptor
(TNFR) superfamily. It is thought to play a role analogous to other
soluble members of the TNFR superfamily by interfering with the ability
of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM and to play a role in
herpes simplex virus (HSV) entry. The invention is based on the discovery
of 3 cDNA molecules (see AAZ94195-97) which encode soluble forms (see
AAZ94195-97), and 1 cDNA molecule (see AAZ94198) that encodes a 2nd
membrane-bound form (see AAZ94198). In addition to isolated
full-length proteins and polynucleotides, and invention provides TANGO-69
-receptor fusion proteins, antigenic peptides and antibodies. Also
provided are recombinant expression vectors, host cells and transgenic
animals in which a TANGO-69-receptor gene has been introduced or
disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be

used in screening and detection assays (e.g. chromosomal mapping, tissue
typing). HVEM proteins can also be used for regulation of cell
proliferation, cell differentiation, cell survival, inflammation mast
cell activity, HSV infection and/or proliferation, and/or coagulation.
HVEM agonists can be used to treat disorders associated with decreased
HVEM activity, e.g. proliferative disorders such as carcinoma or
pathogenic infection. Antagonists can be used to treat disorders
associated with increased HVEM activity, e.g. autoimmune, T cell,
inflammatory and allergic inflammation disorders

Sequence 193 AA;

Query Match 92.9%; Score 1065; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.7e-77;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPPTPTPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECCPKCSFG 60
DB 1 MEPPGDWGPPTPTPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECCPKCSFG 60
QY 61 YRVEACGELTGTVCPCPPGTVIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
DB 61 YRVEACGELTGTVCPCPPGTVIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSPGQVQXGTESDTLQCNCPPTGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSPGQVQXGTESDTLQCNCPPTGTFSPNGTLEECQ 180
QY 181 HQTN 184
DB 181 HQTN 184

RESULT 4

ABU60675

ID ABU60675 standard; protein; 193 AA.

XX AC ABU60675;

DT 06-MAY-2003 (first entry)

DE Human soluble Herpesvirus Entry Mediator-1 (SHVEM-1).

KW Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
SHVEM1; SHVEM2; mHVEM2; tumour necrosis factor receptor; TNFR;
immune disorder; autoimmune disorder; arthritis; graft rejection;
T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
asthma; psoriasis; apototic disorder; rheumatoid arthritis;
systemic lupus erythematosus; insulin-dependent diabetes mellitus;
cytotoxic disorder; septic shock; cachexia; proliferative disorder;
B-cell cancer.

XX OS Homo sapiens.

XX PN US2002132297-A1.

XX ED 19-SEP-2002.

XX PF 21-AUG-2001; 2001US-00934289.

XX PR 03-SEP-1998; 98US-00146950.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ;

XX DR WPI; 2003-255105/25.

XX DR N-PSDB; ABX90556, ABX90557.

XX PT New TANGO-69 receptor polynucleotides and polypeptides, useful for
treating arthritis, graft rejection, AIDS, bacterial infection,

psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

Claim 8; Fig 1; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins sHVM1, sHVM2, sHVM3 and mHVM2 (where HVM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein

Sequence 193 AA;

Query Match 92.9%; Score 1065; DB 6; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.7e-77;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPWPWSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
1 MEPPGDWGPWPWSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
61 YRVKEAGELTGVCEPPTGVTIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEAGELTGVCEPPTGVTIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSTQTLQCNCPPTGTFSPNGTLESCQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSTQTLQCNCPPTGTFSPNGTLESCQ 180
181 HQTN 184
181 HQTN 184

SULT 5
Y79207

AAV79207 standard; protein; 277 AA.

AAV79207;

19-JUN-2000 (first entry)

Membrane-bound herpesvirus entry mediator-2 (mHVM2).

mHVM-2; membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; human; herpes simplex virus; infection; cancer; inflammation; autoimmune disorder; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..38
/note= "signal peptide"
Protein 39..277
/note= "mature protein, also separately claimed in Claim 8"
Domain 42..75

FT Domain /note= "cysteine-rich domain"
FT 78..119
FT /note= "cysteine-rich domain"
FT 110
FT Modified-site /note= "N-glycosylated"
FT 121..162
FT Domain /note= "cysteine-rich domain"
FT 165..186
FT Domain /note= "cysteine-rich domain (partial)"
FT Modified-site 173
FT /note= "N-glycosylated"
FT 201..225
FT Domain /note= "transmembrane domain"

WO200014230-A1.

PD 15-MAR-2000.

PF 03-SEP-1999; 99WO-US020180.

PR 03-SEP-1998; 98US-00146950.

PR 29-JUN-1999; 99US-00342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Busfield SJ;

XX WPI; 2000-256981/22.

DR N-PSDB; AA294198.

XX New nucleic acid molecule encoding herpes virus entry mediator (HVM),
PT either in the soluble or membrane bound form, is useful in screening
PT assays and detection assays.

PS Claim 8; Fig 7; 149pp; English.

XX This polypeptide, the mature portion of which is also claimed, is human
CC membrane-bound herpesvirus entry mediator-2 (mHVM2), a novel form of
CC membrane-bound herpesvirus entry mediator (mHVM). The amino acid
CC sequence was deduced from an isolated cDNA clone (see AA294198). mHVM2
CC is a TANGO-69-receptor and member of the tumour necrosis factor receptor
CC (TNF) superfamily. HVM plays a role in herpes simplex virus (HSV)
CC entry. The invention is based on the discovery of 3 cDNA molecules (see
CC AA294195-97) which encode soluble forms (see AA29204-06) of mHVM, and
CC the cDNA molecule encoding of mHVM2. In addition to isolated full-length
CC proteins and polynucleotides, and invention provides TANGO-69-receptor
CC fusion proteins, antigenic peptides and antibodies. Also provided are
CC recombinant expression vectors, host cells and transgenic animals in
CC which a TANGO-69-receptor gene has been introduced or disrupted. DNA
CC encoding HVM, HVM proteins and HVM antibodies can be used in screening
CC and detection assays (e.g. chromosomal mapping, tissue typing). HVM
CC proteins can also be used for regulation of cell proliferation, cell
CC differentiation, cell survival, inflammation mast cell activity, HSV
CC infection and/or proliferation, and/or coagulation. HVM agonists can be
CC used to treat disorders associated with decreased HVM activity, e.g.
CC proliferative disorders such as carcinoma or pathogenic infection.
CC Antagonists can be used to treat disorders associated with increased HVM
CC activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation
CC disorders

XX Sequence 277 AA;

Query Match 92.5%; Score 1060; DB 3; Length 277;

Best Local Similarity 98.4%; Pred. No. 1.7e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MEPPGDWGPWPWSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60

Db 1 MEPPGDWGPWPWSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60

Qy 61 YRVKEAGELTGVCEPPTGVTIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

Db 61 YRVKEAGELTGVCEPPTGVTIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

Claim 1; Page 47-48; 73pp; English.

The present sequence is the human tumour necrosis factor (TNF) receptor, which may be used for the identification of TNF receptor agonists or antagonists. TNF receptor agonists inhibit tumour growth, stimulate cell (e.g. T cell) differentiation, mediate the immune and antiviral responses, regulate growth, protect against radiation and Chlamydia infection, and can be used to treat immunodeficiencies, e.g. human immunodeficiency virus. Antagonists can be used to treat T cell mediated autoimmune disease, inflammation, septic shock, cerebral malaria, cachexia or B cell cancers, to inhibit graft-host reactions and to prevent apoptosis or cytotoxicity. Fragments of the TNF receptor encoding DNA can be used as hybridisation probes for detecting related genes. Antibodies against the protein can be used as reagents for detecting/measuring soluble forms of protein in the circulation

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSFG 60
1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSFG 60
61 YRVKEACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

SUITE 8

W69238

AAW69238 standard; protein; 283 AA.

AAW69238;

21-OCT-1998 (first entry)

Herpesvirus entry mediator protein.

Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
gene expression regulator; cellular stress; inflammatory response;
lymphocyte activity regulator; autoimmune response.

Homo sapiens.

W09825967-A1.

18-JUN-1998.

05-DEC-1997; 97WO-US022278.

12-DEC-1996; 96US-0032705P.

(GETH) GENENTECH INC.

Ashkenazi AJ, Marsters SA;

WPI; 1998-348457/30.

N-PSDB; AAV44852.

Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for
HVEM and to produce antibodies and transgenic animals, e.g. for drug
screening.

XX

Claim 1; Fig 1; 46pp; English.

This sequence is the herpesvirus entry mediator (HVEM) protein of the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain transacting factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of therapeutically useful reagents

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSFG 60

Db 1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSFG 60

QY 61 YRVKEACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

Db 61 YRVKEACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 9

RAY06488

ID AAY06488 standard; protein; 283 AA.

XX AAY06488;

27-SEP-1999 (first entry)

Human tumour-associated protein PRO509.

PRO1112; UNQ555; cancer; tumour necrosis factor receptor; diagnosis;
therapy; human.

OS Homo sapiens.

Key Location/Qualifiers

Domain 201..225

Domain /note= "transmembrane domain"

Domain 226..283

Domain /note= "cytoplasmic domain"

XX WO9935170-A2.

XX

15-JUL-1999.
 05-JAN-1999; 99WO-US000106.
 05-JAN-1998; 98US-0070440P.
 29-APR-1998; 98US-0083500P.
 22-MAY-1998; 98US-0085414P.
 10-JUN-1998; 98US-0088742P.
 10-NOV-1998; 98US-0107783P.
 20-NOV-1998; 98US-0109304P.
 (GETH) GENENTECH INC.
 Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy WA;
 Wood WI;
 WPI; 1999-430385/36.
 N-P8DB; AAX87265.
 Antibody against proteins expressed in neoplastic cells, useful for tumor
 diagnosis and treatment.
 Example 1; Fig 24; 162pp; English.

This sequence represents human PRO509 (UNQ329), a protein encoded by the
 novel cDNA clone DNA50148 (see AAX87264), and a member of the tumor
 necrosis factor receptor family. Amplification of DNA50148 was observed
 in various tumor tissues, suggesting a role in tumor formation or
 growth. Antagonists (e.g. antibodies) directed to PRO509 may have use in
 cancer therapy. The invention identifies 14 genes (see AAX87254-67) that
 are amplified in the genome of tumor cells. Such amplification is
 expected to be associated with overexpression of the gene product and to
 contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may
 be useful targets for the diagnosis and/or treatment (including
 prevention) of certain cancers, and may act as predictors of the
 prognosis of tumor treatment. Antibodies that bind the proteins are
 claimed and used in claimed cancer diagnostic kits

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
 est Local Similarity 98.4%; Pred. No. 1.8e-76;
 matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 1 MEPPDGDGPPPPWRSTPRDVLRLVLYLTFILGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
 1 MEPPDGDGPPPPWRSTPRDVLRLVLYLTFILGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
 61 YRVKEACGELGTVCBPCPPPTTYIAHLNGLSKLQCOMCDPAMGLRASRNCSTENAVCG 120
 61 YRVKEACGELGTVCBPCPPPTTYIAHLNGLSKLQCOMCDPAMGLRASRNCSTENAVCG 120
 121 CSPGHFCIVQGDHCAACRAVATSSPGORVOKGTESQDTLCONCPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQGDHCAACRAVATSSPGORVOKGTESQDTLCONCPGTFSPNGTLEECQ 180
 181 HQT--NW 185
 181 HQTCSW 187

ULT 10
 94721

AAY94721 standard; protein; 283 AA.

AAY94721;

29-JAN-2001 (first entry)

Human TR2-receptor protein sequence.

Tumour necrosis factor-receptor related protein; TR2; human; cancer;
 chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;

immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
 severely combined immunodeficiency; apoptosis inhibition;
 Alzheimer's disease; Parkinson's disease; Crohn's disease.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..38
 Protein /note= "Signal peptide"
 39..283
 /label= TR2 receptor

WO200056405-A2.

28-SEP-2000.

22-MAR-2000; 2000WO-US007521.

22-MAR-1999; 99US-0125683P.

26-MAR-1999; 99US-0126522P.

20-MAY-1999; 99US-0135169P.

06-AUG-1999; 99US-0147383P.

(NLJJ/) NI J.

(ROSE/) ROSEN C A.

(GENT/) GENTZ R L.

NI J, Rosen CA, Gentz RL;

WPI; 2000-594519/56.

N-P8DB; AAX28149.

Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
 and its two splice variants, useful for treating arthritis or
 inflammation, cancer (such as follicular lymphomas) and immunodeficiency
 disorders.

Disclosure; Page 370; 373pp; English.

This invention relates to an isolated nucleic acid molecule encoding a
 human tumor necrosis factor (TNF)-receptor related protein TR2. Included
 in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
 The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
 member of the TNFR superfamily. The invention includes a method for the
 treatment of arthritis or inflammation using an antibody directed against
 a fragment of the TR2 protein. TR2 its agonists, antagonists and
 antibodies exhibit cytostatic, dermatological, antianemic,
 immunosuppressive, anti-allergic, antiarthritic, antiparkinsonian, and
 antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
 cerebroprotective activity. The methods are useful for treating arthritis
 or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 mutations, cardiac tumors, pancreatic, breast, or prostate cancer), an
 immunodeficiency or for enhancing an in vivo leukocyte response to an
 antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
 dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 inflammatory myopathies) and immunodeficiency disorders (such as severely
 combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
 TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 antagonists are useful for treating or preventing autoimmune diseases and
 inhibit the growth, progression and/or metastasis of cancers. They are
 also used to activate, differentiate or proliferate cancerous cells or
 tissues, and can be used to treat diseases associated with increased cell
 survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 as sources for generating antibodies, as molecular weight markers. This
 sequence represents the TR2 receptor protein of the invention

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 3; Length 283;
 Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLCONCPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLCONCPGTFSPNGTLEECQ 180
 181 HQT--NW 185
 181 HQTCSW 187

SULT 11
 Y95348

AA95348 standard; protein; 283 AA.

AA95348;

25-SEP-2000 (first entry)

Human PRO509 antitumour protein.

PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer;
 ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
 prostate cancer; lung cancer; bladder cancer;
 central nervous system cancer; melanoma; leukaemia; neoplasm.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..36
 Protein 37..283
 /label= Signal_peptide
 /label= PRO509
 Modified-site 81..87
 /note= "N-myristoylation"
 Modified-site 89..95
 /note= "N-myristoylation"
 Modified-site 104..110
 /note= "N-myristoylation"
 Modified-site 110..114
 /note= "Asn is N-glycosylated"
 Modified-site 120..126
 /note= "N-myristoylation"
 Modified-site 153..159
 /note= "N-myristoylation"
 Modified-site 173..177
 /note= "Asn is N-glycosylated"
 Modified-site 192..201
 /note= "N-myristoylation"
 Modified-site 193..199
 /note= "N-myristoylation"
 Domain 205..221
 /note= "transmembrane domain"
 Modified-site 220..226
 /note= "N-myristoylation"
 Region 231..234
 /note= "cell attachment sequence"

WO200037638-A2.

29-JUN-2000.

02-DEC-1999; 99WO-US028565.

22-DEC-1998; 98US-0113296P.

PR 08-MAR-1999; 99WO-US005028.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
 PI Napier MA, Pitti RM, Wood WI;
 XX N-PSDB; AAA49727.
 DR WPI; 2000-442668/38.
 XX Novel composition to inhibit neoplastic cell growth or for treating tumor
 PT in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,
 PT PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866.
 XX Claim 19; Fig 24; 172pp; English.

The present sequence is that of human antitumour protein PRO509, as
 deduced from a retinal cDNA clone (see AAA49727). PRO509 shows homology
 to members of the human tumour necrosis factor receptor family such as
 the lymphotoxin-beta receptor (11 identities) and CD40 (12 identities). A
 claimed method for inhibiting the growth of a tumour cell comprises
 exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221,
 PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see
 AA95337-49), their agonists or chimeric polypeptides incorporating them.
 The tumour is especially a cancer selected from breast, ovarian, renal,
 colorectal, uterine, prostate, lung, bladder and central nervous system
 cancer, melanoma and leukaemia. Methods for the recombinant expression of
 the antitumour proteins are also provided

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 3; Length 283;

Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60

Db 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60

QY 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120

Db 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLCONCPGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLCONCPGTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 12

AA953695

ID AAY93695 standard; protein; 283 AA.

XX AAY93695;

XX 03-OCT-2000 (first entry)

XX Amino acid sequence of novel polypeptide PRO509.

XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715;

XX PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis;

XX cancer; neoplastic cell growth; cell proliferation.

XX

Homo sapiens.

Key Peptide Location/Qualifiers
1...36 "signal sequence"
81...87
Modified-site /note= "N-myristoylation site"
89...95
Modified-site /note= "N-myristoylation site"
104...110
Modified-site /note= "N-myristoylation site"
110...114
Modified-site /note= "N-glycosylation site"
120...126
Modified-site /note= "N-myristoylation site"
153...159
Modified-site /note= "N-myristoylation site"
173...177
Modified-site /note= "N-glycosylation site"
193...199
Modified-site /note= "N-myristoylation site"
195...201
Modified-site /note= "N-myristoylation site"
203...222
Domain /note= "transmembrane domain"
Modified-site 220...226
Region /note= "N-myristoylation site"
231...234
/note= "cell attachment sequence"

WO200037640-A2.

29-JUN-2000.

16-DEC-1999; 99WO-US030095.

22-DEC-1998; 98US-0113296P.

08-MAR-1999; 99WO-US005028.

02-JUN-1999; 99WO-US012252.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021090.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

02-DEC-1999; 99WO-US028565.

(GETH) GENENTECH INC.

Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
Wood WI;

WPI; 2000-452188/39.

N-PSDB; AAA46931.

New anti-polypeptide antibody useful in the treatment and diagnosis of
neoplastic cell growth and proliferation.

Claim 61; Fig 24; 220pp; English.

The present sequence represents a novel human polypeptide. The
specification describes novel polypeptides designated PRO201, PRO292,
PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017,
PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the
genome of tumour cells. The polypeptides are believed to contribute to
tumorigenesis. The polypeptides are useful target for the identification
of certain cancers, and may act as predictors of the prognosis of tumour
treatment. Antibodies against these polypeptides are useful in the
treatment and diagnosis of neoplastic cell growth and proliferation in
mammals

Sequence 283 AA;

very Match 92.5%; Score 1060; DB 3; Length 283;

Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGMGPPFMRSTPRDVLRLVLYTLFLGAPCYAPALPESCKEDYFVVGSECCPKCSGP 60

Db 1 MEPPDGMGPPFMRSTPRDVLRLVLYTLFLGAPCYAPALPESCKEDYFVVGSECCPKCSGP 60

QY 61 YRVKEACGLTGTVCPCPPGTIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120

Db 61 YRVKEACGLTGTVCPCPPGTIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120

QY 121 CSPGHFCIVQGDHCAACRAYATSSPQVRVQKGTESQDTLCQCPGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQGDHCAACRAYATSSPQVRVQKGTESQDTLCQCPGTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 13

AAE20852

ID AAE20852 standard; protein; 283 AA.

XX AC AAE20852;

XX DT 01-JUL-2002 (first entry)

XX DE Human tumour necrosis factor receptor (TNFR) related protein.

XX KW Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;

XX KW immune system-related disorder; inflammatory disease; immunosuppressive;

XX KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;

XX KW autoimmune disease; Crohn's disease; rheumatoid arthritis;

XX KW multiple sclerosis; Systemic lupus erythematosus; rheumatoid arthritis;

XX KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;

XX KW neuroprotective; antiarteriosclerotic; dermatological; aschna.

XX OS Homo sapiens.

XX PN WO200218622-A2.

XX PD 07-MAR-2002.

XX PF 24-AUG-2001; 2001WO-US026396.

XX PR 25-AUG-2000; 2000US-0227598P.

XX PR 21-NOV-2000; 2000US-0252131P.

XX PR 06-JUL-2001; 2001US-0303224P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Feng P;

XX DR WPI; 2002-281068/32.

XX PT Novel nucleic acid molecules comprising a polynucleotide encoding human

XX PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides

XX XX useful for treating disease e.g. inflammatory and autoimmune disorders.

XX Claim 36; Page 346-347; 350pp; English.

XX The invention relates to human tumour necrosis factor receptor (TNFR)-

XX 6alpha and 6beta protein and their corresponding nucleic acids. The

XX invention provides screening methods for identifying agonists and

XX antagonists of TNFR-6alpha and 6beta activity. The invention also

XX provides diagnostic and therapeutic methods for detecting and treating

XX immune system-related disorders. The method is useful for treating or

XX preventing an inflammatory disease or disorder selected from bowel

XX disease, encephalitis, atherosclerosis and psoriasis; an autoimmune

XX disease or disorder selected from systemic lupus erythematosus,

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

XX Crohn's disease, and

or asthma. The present sequence is human TNFR-6alpha and TNFR-6beta related protein

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 5; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSG 60
1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSG 60
61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
121 CSPGHFCIVQDGHCAACRAVATSSPQQRVQKGTESQDTLQCNCPPTFSPNGTLEECQ 180
121 CSPGHFCIVQDGHCAACRAVATSSPQQRVQKGTESQDTLQCNCPPTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

RESULT 14

ABU0681

ABU0681 standard; protein; 283 AA.

ABU0681;

06-MAY-2003 (first entry)

Human membrane-bound Herpesvirus Entry Mediator (mHVEM).

Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM; SHVEM1, SHVEM2, SHVEM3, mHVEM2; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicemia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder; asthma; psoriasis; apoptotic disorder; rheumatoid arthritis; systemic lupus erythematosus; insulin-dependent diabetes mellitus; cytotoxic disorder; septic shock; cachexia; proliferative disorder; B-cell cancer.

Homo sapiens.

US2002132297-A1.

19-SEP-2002.

21-AUG-2001; 2001US-00934289.

03-SEP-1998; 98US-00146950.

(MILL-) MILLENNIUM PHARM INC.

Busfield S7;

WPI; 2003-255106/25.

N-PSDB; ABX90562.

New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

Disclosure; Fig 10; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion

of the proteins SHVEM1, SHVEM2, SHVEM3 and mHVEM2 (where HVEM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to the and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancer). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 6; Length 283;

Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSG 60

Db 1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSCECPKCSG 60

QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120

Db 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120

QY 121 CSPGHFCIVQDGHCAACRAVATSSPQQRVQKGTESQDTLQCNCPPTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQDGHCAACRAVATSSPQQRVQKGTESQDTLQCNCPPTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 15

ABR58631

ID ABR58631 standard; protein; 283 AA.

AC ABR58631;

DT 09-JUL-2003 (first entry)

DE Human cancer related protein SEQ ID NO:288.

Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

heart disease; atherosclerosis; endometriosis.

OS Homo sapiens.

FN WO2003025138-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-US029560.

PR 17-SEP-2001; 2001US-0323469P.

PR 13-NOV-2001; 2001US-0323887P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

PA

XX

Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
Zlotnick A;

WPI; 2003-354600/33.
N-PSDB; ACC72778.

New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.

Claim 12; Page 750; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72880 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

Sequence 283 AA;

Very Match 92.5%; Score 1060; DB 6; Length 283;
1st Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPGDWGPFPWRSTPRDVLRLVLYLTLFGAPCYAPALPCKEDYVVGSCCPKCSFG 60
1 MEPPGDWGPFPWRSTPRDVLRLVLYLTLFGAPCYAPALPCKEDYVVGSCCPKCSFG 60
61 YRVKEACGELTGTVCEPCPGTGTIAHNLGLSKLQCMCDPAWGLRASNCRSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTGTIAHNLGLSKLQCMCDPAWGLRASNCRSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

ch completed: June 10, 2004, 12:31:36
time : 97 secs

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protein - protein search, using sw model

on: June 10, 2004, 12:31:43 ; Search time 46 seconds
(without alignments)
221.094 Million cell updates/sec

le: US-09-934-289A-18

fect score: 1146
uence: 1 MEPPDGDWGPWPWRSTPRTDV.....ECQHQTWPNHMCCKKXAG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

urched: 389414 seqs, 51625971 residues

al number of hits satisfying chosen parameters: 389414

imum DB seq length: 0

cimum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/ECTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query	Match	Length	DB	ID	Description
1	1146	100.0	197	3	US-09-146-950-18		Sequence 19, Appl
2	1065	92.9	193	3	US-09-146-950-2		Sequence 2, Appl
3	1060	92.5	283	3	US-08-503-024-2		Sequence 2, Appl
4	1060	92.5	283	4	US-09-333-279-2		Sequence 2, Appl
5	1060	92.5	283	4	US-09-631-780-2		Sequence 2, Appl
6	1060	92.5	419	3	US-08-503-024-7		Sequence 7, Appl
7	1060	92.5	419	4	US-09-333-279-7		Sequence 7, Appl
8	1060	92.5	419	4	US-09-631-780-7		Sequence 7, Appl
9	1054	92.0	283	4	US-09-072-993C-2		Sequence 2, Appl
10	1052	91.8	283	5	PCT-US96-12174-2		Sequence 2, Appl
11	925	80.7	159	3	US-09-146-950-20		Sequence 20, Appl
12	844	73.6	155	3	US-09-146-950-4		Sequence 4, Appl
13	802.5	70.0	161	4	US-09-523-323-56		Sequence 56, Appl
14	451	39.4	77	3	US-09-146-950-25		Sequence 25, Appl
15	261	22.8	207	3	US-08-974-022-47		Sequence 47, Appl
16	261	22.8	207	3	US-08-795-445A-47		Sequence 47, Appl
17	261	22.8	207	3	US-08-795-447A-47		Sequence 47, Appl
18	261	22.8	207	3	US-08-974-186-47		Sequence 47, Appl
19	261	22.8	207	3	US-08-795-446B-47		Sequence 47, Appl
20	261	22.8	207	4	US-08-706-945D-133		Sequence 133, App
21	261	22.8	207	4	US-08-577-788C-47		Sequence 47, Appl
22	261	22.8	325	1	US-08-292-549-2		Sequence 2, Appl
23	261	22.8	325	3	US-09-043-785A-9		Sequence 9, Appl
24	261	22.8	325	5	PCT-US91-02207-2		Sequence 2, Appl
25	259	22.6	45	3	US-09-146-950-9		Sequence 9, Appl
26	259	22.6	227	3	US-08-574-022-48		Sequence 48, Appl
27	259	22.6	227	3	US-08-795-445A-48		Sequence 48, Appl

28 259 22.6 227 3 US-08-795-447A-48 Sequence 48, Appl
29 259 22.6 227 3 US-08-974-186-48 Sequence 48, Appl
30 259 22.6 227 3 US-08-795-446B-48 Sequence 48, Appl
31 259 22.6 227 4 US-08-706-945D-134 Sequence 134, App
32 259 22.6 227 4 US-08-577-788C-48 Sequence 48, Appl
33 259 22.6 235 4 US-09-326-394-4 Sequence 4, Appl
34 259 22.6 235 4 US-09-580-235-4 Sequence 4, Appl
35 259 22.6 235 4 US-09-580-235-8 Sequence 8, Appl
36 259 22.6 235 4 US-09-580-181-4 Sequence 4, Appl
37 259 22.6 235 4 US-09-580-181-8 Sequence 8, Appl
38 259 22.6 235 4 US-09-102-530-4 Sequence 4, Appl
39 259 22.6 235 4 US-09-102-530-8 Sequence 8, Appl
40 259 22.6 257 4 US-09-579-845-10 Sequence 10, Appl
41 259 22.6 461 1 US-08-385-223-2 Sequence 2, Appl
42 259 22.6 461 2 US-08-650-000-2 Sequence 2, Appl
43 259 22.6 461 3 US-09-042-785A-7 Sequence 7, Appl
44 259 22.6 461 3 US-08-477-347-3 Sequence 3, Appl
45 259 22.6 461 3 US-09-006-353A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-146-950-18
; Sequence 18, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-18

Query Match 100.0%; Score 1146; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 9.6e-96;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGDWGPWPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
DB 1 MEPPDGDWGPWPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
QY 61 YRVKACGELGTVCCEPCPGTYTAHLNGLSKLCQCOMCDPAMGLRASRNCSTRTEAVCG 120
DB 61 YRVKACGELGTVCCEPCPGTYTAHLNGLSKLCQCOMCDPAMGLRASRNCSTRTEAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAVATSSPGQVKGSTESQDTLCQCPPTSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAVATSSPGQVKGSTESQDTLCQCPPTSPNGTLEECQ 180
QY 181 HQTWPNHMCCKKXAG 197
DB 181 HQTWPNHMCCKKXAG 197

RESULT 2

US-09-146-950-2
; Sequence 2, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A


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CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
-09-146-950-2

Query Match      92.9%; Score 1065; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
181 HQTN 184
181 HQTN 184

SULT 3
-08-509-024-2
Sequence 2, Application US/08509024B
Patent No. 6291207
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/08/509,024B
CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
-08-509-024-2

Query Match      92.5%; Score 1060; DB 3; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
181 HQTN 184
181 HQTN 184

SULT 4
-09-333-279-2
Sequence 2, Application US/09333279
```

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; Patent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/09/333,279
; CURRENT FILING DATE: 1999-05-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-279-2

Query Match      92.5%; Score 1060; DB 4; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
DB 1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
QY 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
DB 181 HQTCSW 187

RESULT 5
US-09-631-780-2
Sequence 2, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-2

Query Match      92.5%; Score 1060; DB 4; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
DB 1 MEPPGDMGPPPPWRRTPRTDVLRLVLYTLFLGAPCYAPALPSCCKEDYFVGSECCPKCSPG 60
QY 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
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181 HOT--NW 188
 181 HQTCSW 187

08-509-024-7
 sequence 7, Application US/08509024B
 Patent No. 6291207
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/08/509,024B
 PRIOR FILING DATE: 1995-07-25
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent In Ver. 2.0
 EQ ID NO 7
 LENGTH: 419
 TYPE: PRT
 ORGANISM: Homo sapiens
 08-509-024-7

Query Match 92.5%; Score 1060; DB 3; Length 419;
 Best Local Similarity 97.9%; Pred. No. 1.2e-87;
 Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQTWPNH 188
 181 HQTCKRIH 188

09-333-279-7
 sequence 7, Application US/09333279
 Patent No. 6303336
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/09/333,279
 PRIOR FILING DATE: 1999-06-15
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent In Ver. 2.0
 EQ ID NO 7
 LENGTH: 419
 TYPE: PRT
 ORGANISM: Homo sapiens
 09-333-279-7

Query Match 92.5%; Score 1060; DB 4; Length 419;
 Best Local Similarity 97.9%; Pred. No. 1.2e-87;
 Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQTWPNH 188
 181 HQTCKRIH 188

61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQTWPNH 188
 181 HQTCKRIH 188

RESULT 8
 US-09-631-780-7
 ; Sequence 7, Application US/09631780
 ; Patent No. 6573058
 ; GENERAL INFORMATION:
 ; APPLICANT: SPEAR, Patricia G.
 ; APPLICANT: MONTGOMERY, Rebecca I.
 ; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 ; FILE REFERENCE: 0290-1
 ; CURRENT APPLICATION NUMBER: US/09/631,780
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US/08/509,024B
 ; PRIOR FILING DATE: 1995-07-25
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-631-780-7

Query Match 92.5%; Score 1060; DB 4; Length 419;
 Best Local Similarity 97.9%; Pred. No. 1.2e-87;
 Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 1 MEPPGDGPPPPWSTPRDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 61 YRVEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQTWPNH 188
 181 HQTCKRIH 188

RESULT 9
 US-09-072-993C-2
 ; Sequence 2, Application US/09072993C
 ; Patent No. 6346388
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael R. Brigham-Burke
 ; APPLICANT: Peter R. Young
 ; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
 ; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
 ; FILE REFERENCE: GH-50030
 ; CURRENT APPLICATION NUMBER: US/09/072,993C
 ; CURRENT FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/055,513
 ; PRIOR FILING DATE: 1997-08-13
 ; PRIOR APPLICATION NUMBER: 60/056,980
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/057,550
 ; PRIOR FILING DATE: 1997-08-29

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NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: HOMO SAPIENS
-09-072-993C-2

Query Match          92.0%; Score 1054; DB 4; Length 283;
Best Local Similarity 97.9%; Pred. No. 2.7e-87;
Matches 183; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCMDPAMGLRASNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCMDPAMGLRASNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

RESULT 10
T-US96-12374-2
Sequence 2, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas B.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
T-US96-12374-2

Query Match          91.8%; Score 1052; DB 5; Length 283;
Best Local Similarity 97.3%; Pred. No. 4.1e-87;
Matches 182; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
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Db          1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
QY          61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCMDPAMGLRASNCSTENAVCG 120
Db          61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCMDPAMGLRASNCSTENAVCG 120
QY          121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
Db          121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
QY          181 HQT--NW 185
Db          181 HQTCSW 187

RESULT 11
US-09-146-950-20
Sequence 20, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-20

Query Match          80.7%; Score 925; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.7e-76;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          39 LPSCKEDEYPVGSCECCPKCSPGYRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCM 98
Db          1 LPSCKEDEYPVGSCECCPKCSPGYRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCCM 60
QY          99 CDPAMGLRASNCSTENAVCGSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQ 158
Db          61 CDPAMGLRASNCSTENAVCGSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQ 120
QY          159 DTLQCNCPPTGTFSPNGTLEECQDTWPNHMCCKKAKG 197
Db          121 DTLQCNCPPTGTFSPNGTLEECQDTWPNHMCCKKAKG 159

RESULT 12
US-09-146-950-4
Sequence 4, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-4

Query Match          73.6%; Score 844; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
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atches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

39 LPSCKEDEVVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 98
1 LPSCKEDEVVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 60

99 CDPAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 158
61 CDPAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 120

159 DTLQCNCPGTFSPNGTLBECQHOTN 184
121 DTLQCNCPGTFSPNGTLBECQHOTN 146

SULT 13
Sequence 56, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 56
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
-09-523-323-56

Query Match 70.0%; Score 802.5; DB 4; Length 161;
Best Local Similarity 95.9%; Pred. No. 66-65;
Matches 141; Conservative 1; Mismatches 2; Indels 3; Gaps 2;

41 SCHEDEVVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 100
1 SCHEDEVVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 60

101 PAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 160
61 PAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 119

QY 161 LCONCPGTFSPNGTLBECQHOT--NW 185
DB 120 LCONCPGTFSPNGTLBECQHOTKCSW 146

RESULT 14
US-09-146-950-25
Sequence 25, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-25

Query Match 39.4%; Score 451; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLBECQ 180
DB 1 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLBECQ 60

QY 181 HOTNWPNEHCKKKAKG 197
DB 61 HOTNWPNEHCKKKAKG 77

RESULT 15
US-08-974-022-47
Sequence 47, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Behavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen, Ltd.

protein - protein search, using sw model

on: June 10, 2004, 12:32:33 ; Search time 1029 Seconds
(without alignments)
53.936 Million cell updates/sec

le: US-09-934-289A-18

fect score: 1146
pence: 1 MEPPDGMGPPWRSTPRDV.....ECQHTWPNHMCCKKXG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1158786 seqs, 28176120 residues

al number of hits satisfying chosen parameters: 1158786

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imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	1146	100.0	197	9	US-09-934-289A-18
2	1055	92.9	193	9	US-09-934-289A-2
3	1055	92.9	193	15	US-10-369-300-9
4	1050	92.5	277	9	US-09-934-289A-42
5	1050	92.5	277	15	US-10-369-300-10
6	1050	92.5	283	9	US-09-924-231-2
7	1050	92.5	283	9	US-09-934-289A-13
8	1050	92.5	283	9	US-09-935-727-31
9	1050	92.5	283	15	US-10-369-300-2
10	1050	92.5	283	15	US-10-418-242-31
11	1050	92.5	419	9	US-09-924-231-7
12	1057	92.2	283	13	US-10-020-787-2
13	1054	92.0	283	13	US-10-066-209-2
14	1053	91.9	186	9	US-09-934-289A-30
15	1053	91.9	186	15	US-10-369-300-11

16	925	80.7	159	9	US-09-934-289A-20	Sequence 20, Appl
17	844	73.6	155	9	US-09-934-289A-4	Sequence 4, Appli
18	839	73.2	219	9	US-09-934-289A-44	Sequence 44, Appl
19	838	73.1	148	9	US-09-934-289A-32	Sequence 32, Appl
20	802.5	70.0	161	15	US-10-375-680-56	Sequence 56, Appl
21	540	47.1	276	15	US-10-369-300-4	Sequence 4, Appli
22	261	22.8	207	11	US-09-405-032-130	Sequence 130, App
23	261	22.8	659	14	US-10-363-427-12	Sequence 12, Appl
24	259	22.6	184	10	US-09-852-455-8	Sequence 8, Appli
25	259	22.6	225	9	US-09-840-795-10	Sequence 10, Appl
26	259	22.6	227	11	US-09-405-032-131	Sequence 131, App
27	259	22.6	235	9	US-09-907-263-4	Sequence 4, Appli
28	259	22.6	235	10	US-09-882-735-16	Sequence 16, Appl
29	259	22.6	235	12	US-10-621-783-4	Sequence 4, Appli
30	259	22.6	235	12	US-10-622-383-4	Sequence 4, Appli
31	259	22.6	235	14	US-10-243-230-4	Sequence 4, Appli
32	259	22.6	235	14	US-10-243-230-8	Sequence 8, Appli
33	259	22.6	235	14	US-10-436-826-75	Sequence 75, Appl
34	259	22.6	257	14	US-10-313-852-10	Sequence 10, Appl
35	259	22.6	257	14	US-10-314-033-10	Sequence 10, Appl
36	259	22.6	439	15	US-10-360-101-226	Sequence 226, App
37	259	22.6	450	9	US-09-768-779A-3	Sequence 3, Appli
38	259	22.6	450	14	US-10-291-480-3	Sequence 2, Appli
39	259	22.6	461	9	US-09-800-909-2	Sequence 4, Appli
40	259	22.6	461	9	US-09-826-212-4	Sequence 2, Appli
41	259	22.6	461	9	US-09-758-124-2	Sequence 17, Appl
42	259	22.6	461	9	US-09-856-056A-17	Sequence 17, Appl
43	259	22.6	461	9	US-09-894-524-17	Sequence 17, Appl
44	259	22.6	461	9	US-09-840-707A-17	Sequence 17, Appl
45	259	22.6	461	9	US-09-800-908-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-934-289A-18
; Sequence 18, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061CPLCN1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(38)
US-09-934-289A-18

Query Match 100.0%; Score 1146; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.5e-89;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEPPDGMGPPWRSTPRDVLRVLVYITFLGAPCYAPALPSCKEDEYFVGSCECPKCSPG	60
Db	1	MEPPDGMGPPWRSTPRDVLRVLVYITFLGAPCYAPALPSCKEDEYFVGSCECPKCSPG	60
QY	61	YVKEACAGELTGTCVCEPCPGTYTAHLNGLSKLQCMQCDPAMGLRASRNCSTRTENAVCG	120
Db	61	YVKEACAGELTGTCVCEPCPGTYTAHLNGLSKLQCMQCDPAMGLRASRNCSTRTENAVCG	120

121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
181 HQTNPWPMCEKKKAG 197
181 HQTNPWPMCEKKKAG 197

RESULT 2

US-09-934-289A-2
Sequence 2, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061C1P1C1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-2

Query Match 92.9%; Score 1065; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
181 HQTNP 184
181 HQTNP 184

RESULT 3

US-10-369-300-9
Sequence 9, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/358,463
PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-300-9

Query Match 92.9%; Score 1065; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
181 HQTNP 184
181 HQTNP 184

RESULT 4

US-09-934-289A-42
Sequence 42, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061C1P1C1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-42

Query Match 92.5%; Score 1060; DB 9; Length 277;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTSPNGTLEECQ 180
181 HQTNP 185

181 HQTCSW 187

SULT 5

-10-369-300-10
Sequence 10, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/358,463
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
-10-369-300-10

Query Match 92.5%; Score 1060; DB 15; Length 277;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQT--NW 185
181 HQTCSW 187

SULT 6

-09-924-231-2
Sequence 2, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
-09-924-231-2

Query Match 92.5%; Score 1060; DB 9; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
DB 181 HQTCSW 187

RESULT 7

US-09-934-289A-13
Sequence 13, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MBIO98-061CPC1N1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-13

Query Match 92.5%; Score 1060; DB 9; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRKEACGELTGTVCPCPPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
DB 181 HQTCSW 187

RESULT 8

US-09-935-727-31
Sequence 31, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2


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; LENGTH: 283
; TYPE: FRT
; ORGANISM: Homo sapiens
US-10-369-300-2

Query Match          92.5%; Score 1060; DB 15; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps.

Qy 1 MEPPGDWGPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCXEDYYPVGSBCCPKCSFG 60
   |||
Db 1 MEPPGDWGPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCXEDYYPVGSBCCPKCSFG 60
   |||

Qy 61 YVKEACGELGTVCPCPGTYTAHLNGLSKLCQCMCDPAMGLRARNCSRTEHAVCG 120
   |||
Db 61 YVKEACGELGTVCPCPGTYTAHLNGLSKLCQCMCDPAMGLRARNCSRTEHAVCG 120
   |||

Qy 121 CSPGHFCIVQGDGHCAACRAYATSPQORVQKGSTESQDTLCQCPPGTFSPNGTLEEQ 180
   |||
Db 121 CSPGHFCIVQGDGHCAACRAYATSPQORVQKGSTESQDTLCQCPPGTFSPNGTLEEQ 180
   |||

Qy 181 HOT--NW 185
   ||| : ||
Db 181 HOTKCSW 187
   ||| : ||

RESULT 10
US-10-418-242-31
; Sequence 31, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta

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1 FILE REFERENCE: PFT451P3
2
3 CURRENT APPLICATION NUMBER: US/10/418,242
4
5 CURRENT FILING DATE: 2003-04-18
6
7 PRIOR APPLICATION NUMBER: 60/373,604
8
9 PRIOR FILING DATE: 2002-04-19
10
11 PRIOR APPLICATION NUMBER: 09/935,727
12
13 PRIOR FILING DATE: 2001-08-24
14
15 PRIOR APPLICATION NUMBER: 60/303,224
16
17 PRIOR FILING DATE: 2001-07-06
18
19 PRIOR APPLICATION NUMBER: 60/252,131
20
21 PRIOR FILING DATE: 2000-11-21
22
23 PRIOR APPLICATION NUMBER: 60/227,598
24
25 PRIOR FILING DATE: 2000-08-25
26
27 PRIOR APPLICATION NUMBER: 09/518,931
28
29 PRIOR FILING DATE: 2000-03-03
30
31 PRIOR APPLICATION NUMBER: 60/168,235
32
33 PRIOR FILING DATE: 1999-12-01
34
35 PRIOR APPLICATION NUMBER: 60/146,371
36
37 PRIOR FILING DATE: 1999-08-02
38
39 PRIOR APPLICATION NUMBER: 60/131,964
40
41 PRIOR FILING DATE: 1999-04-30
42
43 PRIOR APPLICATION NUMBER: 60/131,279

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; PRIOR APPLICATION NUMBER: 601431,279
; PRIOR FILING DATE: 1999-04-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 31
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-31

Query Match          92.5%; Score 1060; DB 15; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1

Qy 1 MPPGDWGGPPPPNRSTRPTDVLRLVLYTLFGAPCYAPALPSCKEDEYFVGSCECCPKCSGP 60
Db 1 MPPGDWGGPPPPNRSTRPTDVLRLVLYTLFGAPCYAPALPSCKEDEYFVGSCECCPKCSGP 60
Ov 61 YRVKACGELTICEVCPGPGTYIAHLNGLSKCLQCQCMCDPAMGLRASRNCSTENAVCG 120

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11 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

ULT 11
09-924-231-7
sequence 7, Application US/09524231
atent No. US2002010264A1
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
09-924-231-7

Query Match 92.5%; Score 1060; DB 9; Length 419;
Best Local Similarity 97.9%; Pred. No. 2.8e-81;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

ULT 12
10-020-787-2
sequence 2, Application US/10020787
Publication No. US20020102258A1
GENERAL INFORMATION:
APPLICANT: Harrop, Jeremy A.
APPLICANT: Holmes, Stephen D.
APPLICANT: Reddy, Manjula P.
APPLICANT: Truneh, Alemseged
TITLE OF INVENTION: Human Tumor Necrosis Factor
Receptor-Like 2 (TR2) Antibodies
FILE REFERENCE: GH50027C1
CURRENT APPLICATION NUMBER: US/10/020,787
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 09/403,815
PRIOR FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/US98/09744
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/046,249
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; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-020-787-2

Query Match 92.2%; Score 1057; DB 13; Length 283;
Best Local Similarity 97.9%; Pred. No. 3.4e-81;
Matches 183; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
DB 1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
QY 61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
DB 181 HQTCSW 187

RESULT 13
US-10-066-209-2
; Sequence 2, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-2

Query Match 92.0%; Score 1054; DB 13; Length 283;
Best Local Similarity 97.9%; Pred. No. 6.1e-81;
Matches 183; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
DB 1 MEPPDGMGPPPPWRSTPTDVLRLVLYTLFAGPCYAPALPSCKEDEVPGSECCPKCSFG 60
QY 61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCCEPPTGTIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAVATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
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181 HQT--NW 185
||| :||
181 HQTCSW 187

!SULT 14

-09-934-289A-30
Sequence 30, Application US/09934289A
Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: M81098-061C1C1M1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 186

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(38)

-09-934-289A-30

Query Match 91.9%; Score 1053; DB 9; Length 186;
Best Local Similarity 99.5%; Pred. No. 4.8e-81;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MEPPGDWGGPPPPWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCCKEYPPVGSCECCPKCSFG 60

1 MEPPGDWGGPPPPWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCCKEYPPVGSCECCPKCSFG 60

61 YRVKEACGELTGTVCCEPFGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

61 YRVKEACGELTGTVCCEPFGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQT 183

181 HQT 183

!SULT 15

-10-369-300-11

Sequence 11, Application US/10369300

Publication No. US20030215442A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher

APPLICANT: Hancock, Wayne

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF

TITLE OF INVENTION: IMMUNE

TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY

FILE REFERENCE: 7853-255

CURRENT APPLICATION NUMBER: US/10/369,300

CURRENT FILING DATE: 2003-02-19

PRIOR APPLICATION NUMBER: 60/358,463

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 186

! TYPE: PRT
! ORGANISM: Homo sapiens
! US-10-369-300-11

Query Match 91.9%; Score 1053; DB 15; Length 186;
Best Local Similarity 99.5%; Pred. No. 4.8e-81;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPPGDWGGPPPPWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCCKEYPPVGSCECCPKCSFG 60

Db 1 MEPPGDWGGPPPPWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCCKEYPPVGSCECCPKCSFG 60

Qy 61 YRVKEACGELTGTVCCEPFGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

Db 61 YRVKEACGELTGTVCCEPFGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

Qy 181 HQT 183

Db 181 HQT 183

Search completed: June 10, 2004, 12:58:46
Job time : 1030 secs

Matches 56; Conservative 22; Mismatches 66; Indels 22; Gaps 6;

QY 35 YAPALPS-CKEDEV--PVGSECCPKCSPGYRVKACAGELTGTVCPEPPGTYIAHLNGLS 91
Db :
32 YAPEGSTCLREYYDQTAAQMCCSKSPGOHAKVFCFKTSVDTCSDCEDSYTQLWNWVP 91
QY 92 KLCQQCMCDPAMGLRASRN-----CSRTENAVCGSPGHFECIVODGDHGCAACRAYATSS 145
Db :
92 ECLSC-----GSCSSDQVETOACTEQNRITCTCRPGMYCALSKOEGGRCLCAPLRKR 144

QY 146 PQQRVQKGATESDQTLQNCPFGTFPS-PNGTLEBCQHQTNPWHMC 190
Db :
145 PGFGVARGPTETSDVVCKPCAPGTFNSTSTDICR-----PHQIC 185

RESULT 3
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C/Accession: A46476, A46515
R/Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A/Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40 gene
A/Reference number: A46476; UID:92105763; PMID:1370315
A/Accession: A46476
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-305 <OR>
A/Cross-references: GB:M83312; NID:g1553058
A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A/Reference number: A46515; UID:93094586; PMID:1281194
A/Accession: A46515
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-287,'LV'<GRI>
A/Cross-references: GB:M83312; NID:g1553058; PID:AAB08705.1; PID:g1553059; GB:M94126; NJ:
A/Experimental source: BALB/c, liver
A/Note: sequence extracted from NCBI backbone (NCBIPI:120357)
C/Comment: For an alternative splice form, see PIR:A46515.
C/Comment: For an alternative splice form, see PIR:A46476.
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: alternative splicing; transmembrane protein
P:105-144/Domain: NGF receptor repeat homology <NGP>

Query Watch 22.4%; Score 256.5; DB 2; Length 305;
Best Local Similarity 34.4%; Pred. No. 1.4e-11;
Matches 53; Conservative 20; Mismatches 72; Indels 9; Gaps 3;

QY 41 SCKDEYPVGSECCPKCSPGYRVKACAGELTGTVCPEPPGTYIAHLNGLSKLQCOWCD 100
Db :
25 TUSDQKYLDGGCDLQOPGSLTSHCTALEKTQCHPDGSGFSAQWNRIRCHQHRHE 84

QY 101 PAMGLASRNCRTENAVCGSPGHFECIVODGDHCAACRAYATSSPGQRVKQGTTESQDT 160
Db :
85 PNQGLRVKKEGTAESDYCTCKEGHCTSKD---CEACAQHTPCIPGFVWMEMATETTD 141

QY 161 LQONCPPGTFSPNGTL-ECCQHQTNWPNHMCCK 193
Db :
142 VCHPCPVGVFFSNQSLLFEKC-----YPMWTSCEDK 170

RESULT 4
T29623
hypothetical protein G2R - variola major virus
C/Species: variola major virus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C/Accession: T29623
R/Messing, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Aubin,

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QY 21 LRLVLYLTLFLGAPC-----YAPALPCKEDEXYVPGSECCPKCSGGYRVKAEAGCEL 70
Db 1 MKSVLYLYLILPLSCIIINGRDAAAPYPNGKCKDTEYKRHLCLCLSCPPGTYASRLCDSK 60
QY 71 TGTVCPEPCPPGYIAHNLGSKCLOQC-MCDPAMGLRASRNCSTENAVCGSGHFCIV 129
Db 61 TNYCTQPCGSGFTGRNNHLPACUSNGRCH--SNQVETRSCNTHNRICSPGYVCLL 118
QY 130 QQGDHCAACRAYATSPGQRVQKGGTESQDTLQNCQPPGTFSFN-GTILECQHOTN 184
Db 119 KGSSGCKACVSTKKGIGVG-SGHTSVGDVICSPGCGTYSHTVSSADKCEPVN 173

RESULT 6
A:G0771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:G29850; PIN:CAA43045.1; PID:G29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <RA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153.180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.2%; Score 254; DB 2; Length 277;
Best Local Similarity 31.1%; Pred. No. 1.9e-11;
Matches 56; Conservative 30; Mismatches 78; Indels 16; Gaps 5;

QY 20 VLRLVLYLTLFLGAPCAPAL-----PSCKEDEXYVPGSECCPKCSGGYRVKAEAGELTGTV 74
Db 1 MWRLPLQCVLMG--CLLVAVHPBPPTAKREKQYLINQQCLSCQPGOKLVSDCTEFTETE 58
QY 75 CBPCPPGYIAHNLGSKCLOQC-MCDPAMGLRASRNCSTENAVCGSGHFCIVQGDGH 134
Db 59 CLPQCESEFLDTWNRKTHCHQKCDPNLGLRVQKGTSETDTICTCEGWHC---TSEA 115
QY 135 CAACRAYATSPGQRVQKGGTESQDTLQNCQPPGTFS-PNGTILECQHOTNWPNHMEKK 193
Db 116 CBSCVLHRSQSGFGVQKQIATGVSDTICEPCPVFFSNVSAFEKCHPWTs-----CETK 170

RESULT 7
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 15-Sep-2003
C;Accession: D72175

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Db 84 HRSSELKQNCPTPTEDTVCQCRPG-TQPR

SH-----KLGVD--- 121

161 LCQNCPPGTFSPNGTLEBCQHTN 184
122 -CVPFPGHFSP-GSNQACKPWTN 143
ULT 11
700
e ox40 protein - mouse
lternate names: Ox40 antigen
pecies: Mus musculus (house mouse)
ate: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 11-Jan-2000
cession: I48700; I48334; S34377
alderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
Immunol. 151, 5261-5271, 1993
itle: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
ference number: I48700; MUID:94044750; PMID:8228223
cession: I48700
tatus: translated from GB/EMBL/DBJ
olecule type: mRNA
esidues: 1-272 <REG>
ross-references: EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G312828
rkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
J. Immunol. 25, 926-930, 1995
itle: Gene structure and chromosomal localization of the mouse homologue of rat Ox40
ference number: I48334; MUID:95255413; PMID:7737295
cession: I48334
tatus: translated from GB/EMBL/DBJ
olecule type: DNA
esidues: 1-14, 'G', 16-272 <REG>
ross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
enetics:
ene: ox40
ntrons: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
uperfamily: CD27 antigen; NGF receptor repeat homology
uery Match 18.5%; Score 211.5; DB 2; Length 272;
est Local Similarity 31.9%; Pred. No. 2.1e-08;
atches 46; Conservative 16; Mismatches 57; Indels 25; Gaps 5;
41 SCKEDEVGSECCPKSPGYRVEACGELGTVCPCFPFTYIAHLNGLSKLQCCQMD 100
26 NCVKTYFSGHKCECCQPGHGVSRCDHTDLCHPCETGFYNEAVN-YDCKQCTQCN 84
101 PAMGLRARNCRSTENAVCGSPGHFCIVQGDHCAACRAYATSSPQRVQKGTSPQDT 160
85 HRSSELKQNCPTQTQVCRCPG-----TQP--RQDSGYKLGVD- 122
161 LCQNCPPGTFSPNGTLEBCQHTN 184
123 -CVPFPGHFSP-GNNQACKPWTN 144
ULT 12
431
e growth factor receptor precursor, low affinity - rat
lternate names: NGF receptor
pecies: Rattus norvegicus (Norway rat)
ate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
cession: A26431; PH1229
adeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
ure 325, 593-597, 1987
itle: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
ference number: A26431; MUID:87115859; PMID:3027580
cession: A26431
olecule type: mRNA
esidues: 1-425 <RAD>
ross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
etis, M.; Tammusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
e 121, 247-254, 1992
itle: Regulatory elements and transcriptional regulation by testosterone and retinoid
ference number: PH1229; MUID:93077038; PMID:1446821
cession: PH1229

A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F1-29/Domain: signal sequence #status predicted <SIG>
F30-425/Product: nerve growth factor receptor #status predicted <NAT>
F30-251/Domain: extracellular #status predicted <EXT>
F33-66/Domain: NGF receptor repeat homology <NG1>
F68-109/Domain: NGF receptor repeat homology <NG2>
F110-148/Domain: NGF receptor repeat homology <NG3>
F150-190/Domain: NGF receptor repeat homology <NG4>
F198-249/Region: serine/threonine-rich
F252-273/Domain: transmembrane #status predicted <MEM>
F274-425/Domain: intracellular #status predicted <INT>
F61/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 18.2%; Score 208; DB 1; Length 425;
Best Local Similarity 30.9%; Pred. No. 5.3e-08;
Matches 59; Conservative 28; Mismatches 76; Indels 28; Gaps 10;
QY 19 DVLRVLVLYTLFGAPCYAPALFSCKEDEVGSECCPKSPGYRVEACGELGTVCPC 78
DB 12 DRLRLLL-LIILGVSS-GGAKETCTGTGLYTHSGECKKACNLGEGVAQPCG-ANQTVCEPC 68
QY 79 PPGYIAHLNGLSKLQCCQMDPAMGLRA-SRCSRTEENAVCGSPGHFCIVQDGD--HC 135
DB 69 LDNVTFSDV--VSATEPKCKTECLGLQMSAPCEVADAVCRCAVGY--QDEETGHC 123
QY 136 AACRAYATSPQRVQKGTSPQDTLQNCPPGTFSP-----PNGTLEBCQHQ--- 182
DB 124 EAC---SVCEVSGSLVFSCQDKQNTVCECPEGTYSDEANHVDPCLPCTVCEDTERGLRE 180
QY 183 -TNWPNWCEK 192
DB 181 CTFWADAECE 191
RESULT 13
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 27-Oct-2003
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenki
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828
R:Kisssonarghis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
A:Reference number: S54816
A:Accession: S54816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>

Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044
;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
;Keywords: cytokine receptor; transmembrane protein
;1-22/Domain: signal sequence #status predicted <SIG>
;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
;40-77/Domain: NGF receptor repeat homology <NG1>
;79-120/Domain: NGF receptor repeat homology <NG2>
;166-203/Domain: NGF receptor repeat homology <NG4>

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Best Local Similarity 28.1%; Pred. No. 1.3e-07;
Matches 52; Conservative 21; Mismatches 90; Indels 22; Gaps 7;

20 VLRLVLYLTELGAPCYAPALPSCKEDEV--PVGSE-----CCPKCSGYRVKEACGE 69
11 VPELQWATGHTVPAQVLTLYKPEPGVECOISYVDRKAQCCAKCPGQVYKFCNK 70
70 LGTVCEPCPPGTYIAHLNGLSKLQCC--QMCDFAMGLRASNCSTENAVCCSPGHFC 127
71 TSDTVACDCEASMTYQVNNQFRTCLSCSSCTTDQVEIRA---CTKQQRVCAACEAGRYC 127
128 IVQ-DGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPGNTFS--ENGTLCECQHTNW 185
128 ALKTHSGRCQCRNLKSGPGFGVASSRAPNGVNLKACAPGTFSDTTSIDVCR----- 182
186 PNHMC 190
183 PHRIC 187

RESULT 14
18854
;Species: Mus musculus (house mouse)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
;Accession: I48854
;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
;Genome 5, 726-727, 1994
;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
;Reference number: I48854; MUID:95178848; PMID:7873884
;Accession: I48854
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-459 <RES>

Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 17.6%; Score 202; DB 2; Length 459;
Best Local Similarity 30.5%; Pred. No. 1.5e-07;
Matches 43; Conservative 19; Mismatches 69; Indels 10; Gaps 5;

53 CCKPCSPGYRVKEACGELTGTVCCEPPGTYIAHLNGLSKLQCC--QMCDFAMGLRASNC 111
39 CCAKCPGPGQVYKFCNKTSIDTVACDCEASMTYQVNNQFRTCLSCSSC--STDQVETAC 96
112 SRTENAVCCSPGHFCIVQ-DGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPGTF 170
97 TKQQRVCAACEAGRYCAKTHSGSCRCQCRNLKSGPGFGVASSRAPNGVNLKACAPGTF 156
171 S-PNGTLCECQHTNPNHMC 190
157 SDTTSIDVCR-----PHRIC 172

RESULT 15
N0006
;Species: Gallus gallus (chicken)
;Alternate names: NGF receptor
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: JN0006; A60504
;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid

Neuron 2, 1123-1134, 1999
A>Title: Structure and developmental expression of the nerve growth factor receptor in the
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A>Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35 'Y', 37-172 'K', 174-275 'S', 277-395 'R', 397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells.
C;Comment: The cytosolic-rich region of the extracellular domain may form part or all of the
C;Superfamily: This protein is thought to form a high-affinity receptor when it associates with
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.4%; Score 199; DB 1; Length 416;
Best Local Similarity 31.7%; Pred. No. 2.3e-07;
Matches 53; Conservative 26; Mismatches 66; Indels 22; Gaps 9;

QY 37 PALPS-----CKEDYFVSGSECCPKCSGYRVKEACGELTGTVCCEPPG-TYIAHLNG 89
DB 13 PAGPTWGSKEKCLTKMYTTSGECCACNLGEGVQPG-VNQTVCPELDSVTYSPTVSA 71
QY 90 LSKCLQCCQCDPAMGLRA-SRNCSTENAVCCSPGHFCIVQGDHCAACRAYATSSPGQ 148
DB 72 TEPCKPCTQC---VGLHSMFAFCVSDAVCRCAAYGF---QD-ELSGSKCEKSCICEVGF 124
QY 149 RVQKGTESQDTLQCNCPGTFSPNGT-LEECQHTNPNHMCCKK 194
DB 125 GLMFPCRDSDTVCECPGTFSDANFVDFC-----LPCTICEENE 166

Search completed: June 10, 2004, 12:35:00
Job time : 47 secs

GenCore version 5.1.6
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protein - protein search, using sw model

n on: June 10, 2004, 11:06:27 ; Search time 38 Seconds
(without alignments)
269,943 Million cell updates/sec

tle: US-09-934-289A-18

ffect score: 1146

quence: 1 MEPPGDWGPWPWRSTPTDV.....ECQHTNPNHMCCKKAKG 197

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 141681 seqs, 52070155 residues

tal number of hits satisfying chosen parameters: 141681

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	1057	92.2	283	1	TR14_HUMAN
2	266.5	23.3	349	1	CRMB_CAMPS
3	261	22.8	325	1	VT2_SFVKA
4	259	22.6	461	1	TR1B_HUMAN
5	256.5	22.4	289	1	TNR5_MOUSE
6	254.5	22.2	349	1	CRMB_YARV
7	254	22.2	277	1	TNR5_HUMAN
8	243.5	21.2	351	1	CRMB_COWPX
9	242	21.1	269	1	TNR5_BOVIN
10	239.5	20.9	435	1	TNR3_HUMAN
11	238	20.8	326	1	VT2_MXVL
12	236.5	20.6	271	1	TNR4_RAT
13	231	20.2	300	1	TR6B_HUMAN
14	218	19.0	417	1	TR16_MOUSE
15	217	18.9	415	1	TNR3_MOUSE
16	211.5	18.5	272	1	TNR4_MOUSE
17	208	18.2	425	1	TR16_RAT
18	203	17.7	474	1	TR1B_MOUSE
19	202	17.6	332	1	TNR6_PIG
20	199	17.4	416	1	TR16_CHICK
21	198.5	17.3	327	1	TNR6_MOUSE
22	197	17.2	324	1	TNR6_RAT
23	197	17.2	401	1	T11B_HUMAN
24	196.5	17.1	427	1	TR16_HUMAN
25	196	17.1	401	1	T11B_MOUSE
26	193	16.8	401	1	T11B_RAT
27	192	16.8	655	1	TR21_HUMAN
28	190	16.6	616	1	TR11_HUMAN
29	189	16.5	655	1	TR21_MOUSE
30	188.5	16.4	277	1	TNR4_HUMAN
31	186	16.2	417	1	TR25_HUMAN
32	183.5	16.0	335	1	TNR6_HUMAN
33	183	16.0	323	1	TNR6_BOVIN

34	182.5	15.9	625	1	TR11_MOUSE
35	180	15.7	204	1	TR26_MOUSE
36	178.5	15.6	250	1	TNR7_MOUSE
37	169.5	14.8	256	1	TNR9_MOUSE
38	169.5	14.8	454	1	TR1A_MOUSE
39	169	14.7	461	1	TR1A_PIG
40	168	14.7	471	1	TR1A_BOVIN
41	165.5	14.4	461	1	TR1A_RAT
42	164	14.3	498	1	TNR8_MOUSE
43	160	14.0	595	1	TNR8_HUMAN
44	157.5	13.7	176	1	TR23_MOUSE
45	155	13.5	198	1	TR22_MOUSE

ALIGNMENTS

RESULT 1
TR14_HUMAN
ID TR14_HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q8WXR1; Q96J31; Q9UM65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE (Tr2).
GN TNFRSF14 OR HVEM OR HVFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
CX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=37053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
[2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97306336; PubMed=9162061;
RX Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
Porter T.G., Truneh A., Young P.R.;
RA "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RL J. Biol. Chem. 272:14272-14276(1997).
[3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
RX MEDLINE=21629477; PubMed=11756979;
RA Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,
Spear P.G.;
RT "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL J. Infect. Dis. 185:36-44(2002).
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[6]

INTERACTION WITH TRAF2 AND TRAF5.
MEDLINE=97298041; PubMed=9153189;
Hsu H., Soloviyev I., Colombero A., Elliott R., Kelley M., Boyle W.J., "ATAR, a novel tumor necrosis factor receptor family member, signals through TRAF2 and TRAF5", J. Biol. Chem. 272:13471-13474 (1997).

[7]

INTERACTION WITH TRAF3 AND TRAF5.
MEDLINE=97306297; PubMed=9162022;
Masters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M., Ashkenazi A., "Herpesvirus entry mediator, a member of the tumor necrosis factor receptor (TNFR) family, interacts with members of the TNFR-associated factor family and activates the transcription factors NF-kappaB and AP-1.", J. Biol. Chem. 272:14029-14032 (1997).

[8]

X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
MEDLINE=21403268; PubMed=11511370;
Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H., Eisenberg R.J., Wiley D.C., "Herpes simplex virus glycoprotein D bound to the human receptor HveA.", Mol. Cell 8:169-179 (2001).

-!- FUNCTION: Receptor for TNFRSF14/LIGHT and homotrimeric TNFRSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays an important role in HSV pathogenesis because it enhanced the entry of several wildtype HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated human T cells.

-!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.

-!- SUBCELLULAR LOCATION: Type I membrane protein. (Probable).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.

-!- SIMILARITY: Contains 3 TNFR-Cys repeats.

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EMBL; U70321; AAB58354.1; -;
EMBL; U81232; AAD00505.1; -;
EMBL; AF153378; AAF78588.1; -;
EMBL; AF373877; AAL47717.1; -;
EMBL; AF373878; AAL47718.1; -;
EMBL; BC002794; AAR02794.1; -;
PDB; 1JMA; 26-SEP-01.
Genew; HGNC:11912; TNFRSF14.
MIM; 602746; -;
GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
R; GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
R; GO; GO:0006955; P:immune response; TAS.
R; InterPro; IPR008063; Fas_receptor.
R; InterPro; IPR01368; TNFR_c6.
R; Pfam; PF00020; TNFR_c6; 3.
R; PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; Transmembrane; Glycoprotein; Repeat; signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 283 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 39 202 SUPERFAMILY MEMBER 14.
FT TRANSMEM 203 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 224 283 POTENTIAL.
FT REPEAT 42 75 CYTOPLASMIC (POTENTIAL).
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 121 162 TNFR-CYS 2.
FT DISULFID 42 53 TNFR-CYS 3.
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT VARIANT 17 17
FT VARIANT 241 241
FT VARIANT 241 241
FT TURN 44 45
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Query Match 92.2%; Score 1057; DB 1; Length 283;
Best Local Similarity 97.9%; Pred. No. 2.7e-80;
Matches 183; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPFPPESTPTDVLRLVLYLFLGAPCYAPALPCKEDEVPGSECCPKCSPG 60
Db 1 MEPPGDWGPFPPESTPTDVLRLVLYLFLGAPCYAPALPCKEDEVPGSECCPKCSPG 60

QY 61 YRKEACGELTGVCPCPGTYIAHNLGSKLQCCQCDPAMGLRASNCRSTENAVCG 120
Db 61 YRKEACGELTGVCPCPGTYIAHNLGSKLQCCQCDPAMGLRASNCRSTENAVCG 120

QY 121 CSPGHFCTVQDGDHCAACRAYATSPGQGVKGGTQTLQCNCPPGTTFSPNGTLEECQ 180
Db 121 CSPGHFCTVQDGDHCAACRAYATSPGQGVKGGTQTLQCNCPPGTTFSPNGTLEECQ 180

QY 181 HOT--NW 185
Db 181 HQTCKSW 187

RESULT 2
CRME_CAMPS

CRME_CAMPS	STANDARD;	PRT;	349 AA.
Q8UVA7;			
28-FEB-2003 (Rel. 41, Created)			
28-FEB-2003 (Rel. 41, Last sequence update)			
28-FEB-2003 (Rel. 41, Last annotation update)			
Soluble TNF receptor II precursor (cytokine response modifying protein B).			
(CRME1 OR CMP2L OR CMLV002) AND (CRME2 OR CMP205R OR CMLV210).			
Camelpox virus (strain CMS), and			
Camelpox virus (strain M-96).			
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
Orthopoxvirus.			
NCBI_TaxID=203172, 203173;			
[1]			
SEQUENCE FROM N.A.			
STRAIN=M-96;			
Afonso C.L., Tulman B.R., Lu Z., Zeak L., Zaitsev V.L.,			
Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;			
"The genome of camelpox virus."			
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to			
the modification of TNF-mediated antiviral processes (By			
similarity).			
-!- SUBCELLULAR LOCATION: Secreted (By similarity).			
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.			
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or send an email to license@isb-sib.ch).			
EMBL; AY009089; A837456.1; -			
EMBL; AY009089; A837718.1; -			
EMBL; AF438165; AAL73920.1; -			
EMBL; AF438165; AAL73917.1; -			
InterPro; IPR001368; TNFR_C6.			
Pfam; PF00020; TNFR_C6; 2.			
SMART; SM00208; TNFR; 3.			
PROSITE; PS00652; TNFR_NGFR_1; 2.			
PROSITE; PS00050; TNFR_NGFR_2; 2.			
Receptor; Glycoprotein; Repeat; Signal.			
SIGNAL			
CHAIN			
REPEAT			
REPEAT			
REPEAT			
DISULFID			
DISULFID			
DISULFID			
DISULFID			
DISULFID			
DISULFID			
CARBOHYD			
CARBOHYD			
CARBOHYD			
SEQUENCE			
349 AA; 38064 MW; EA412AF991E087F3 CRC64;			
Query Match			
33.1%; Score 266.5; DB 1; Length 349;			
Best Local Similarity			
33.1%; Pred. No. 4.2e-15;			
Matches			
57; Conservative			
24; Mismatches			
15; Gaps			
5;			
21 LRUVLYTLFLGAPC-----YAPALPSCKEDYEVPGSECPKSPGYRKEAGGEL 70			

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Query Match      23.3%; Score 266.5; DB 1; Length 349;  
Best Local Similarity 33.1%; Pred.No. 4.2e-15;  
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;
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DISULFID 86 104 BY SIMILARITY.
DISULFID 106 120 BY SIMILARITY.
DISULFID 123 146 BY SIMILARITY.
DISULFID 129 149 BY SIMILARITY.
DISULFID 164 185 BY SIMILARITY.
CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 325 AA; 35132 MW; 8105303198A71E CRC64;
Query Match 22.8%; Score 261; DB 1; Length 325;
Best Local Similarity 33.3%; Pred. No. 1.1e-14;
Matches 58; Conservative 23; Mismatches 81; Indels 12; Gaps 6;
20 VLRLVLYLFLGAPFCVAPALP-----SKDEYFVSGCEPKSPGVRVKEACGELTGT 73
1 MLRLIALLVCV-VYVYGDVVPYSSNOGKGHDYBKGLCCASCHPQFYASRLCGPGSNT 59
74 VCBPCPPGTVIAHLNGLSKLQCMCDPAMG-LRASRNCSTENAVCGCPGHCIVQDG 132
60 VCSPECDGTSTASTHAPACVSCR--GPTGHLSESQCDRTHDVCNCSGNYCLLKGQ 117
133 DHCACRAYATSPGVRVKGSTESQDILCQCPPTSPN-GILECQHQGTNW 195
118 NGCRIC-APQTKPCAGYGVSGHTRAGDTLCEKCPHTYSDSLSPTRCGTSFNY 170
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
TISSUE=PNS;
MEDLINE=22389257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.K., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchéz A.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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SEQUENCE OF 37-461 FROM N.A.
MEDLINE=91370690; PubMed=1966549;
Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
Brockhaus M., Lesslauer W.,
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intracellular, domain sequences.";
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[7]
SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
MEDLINE=90349572; PubMed=2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
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"Complementary DNA cloning of a receptor for tumor necrosis factor
and demonstration of a shed form of the receptor.";
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SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
MEDLINE=21069356; PubMed=11197692;
Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.,
"New single nucleotide polymorphisms in the coding region of human
TNFR2: association with systemic lupus erythematosus.";
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SEQUENCE OF 27-31.
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urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors.";
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SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
MEDLINE=91056048; PubMed=2173696;
Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
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distinct tumor necrosis factor receptors from HL60 cells.";
J. Biol. Chem. 265:20131-20138 (1990).
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CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddel D.V.,
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Characterization of ligand binding, internalization, and receptor
phosphorylation.";
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"Involvement of CRAF1, a relative of TRAF, in C940 signaling.";
Science 267:1494-1498(1995).
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INTERACTION WITH TRAF5.
MEDLINE=96382484; PubMed=8790348;
Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
Yamamoto T., Inoue J.-I.;
"TRAF5, a novel tumor necrosis factor receptor-associated factor
family protein, mediates CD40 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
-!- FUNCTION: Receptor for TNFSF5/CD40L.
-!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
TRAF2 AND TRAF6 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
and V); secreted (isoform II).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
Name=I;
IsoId=P27512-1; Sequence=Displayed;
Name=II;
IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
Name=III;
IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
Name=IV;
IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
Name=V;
IsoId=P27512-5; Sequence=VSP_006476;
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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or send an email to license@isb-sib.ch).

EMBL; M8312; AAB08705.1; -;
EMBL; M94126; AAA37404.1; -;
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
EMBL; AJ401387; CAC29427.1; -;
EMBL; AJ401388; CAC29428.1; -;
EMBL; AJ401389; CAC29429.1; -;
EMBL; AJ401390; CAC29430.1; -;
PIR; A46476; A46476.
HSP; P25942; ICDF.
MGD; MGI.88336; Tnfrsf5.
InterPro; IPR008063; Fas_receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS0050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
Alternative splicing.
SIGNAL 1 19
CHAIN 20 289

POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 5
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

DOMAIN 20 193
TRANSMEM 194 215
DOMAIN 216 289
REPEAT 25 60
REPEAT 61 103
REPEAT 104 144
REPEAT 145 187
DISULFID 26 37
DISULFID 38 51
DISULFID 41 59

FT	DISULFID	62	77	BY SIMILARITY.
FT	DISULFID	83	103	BY SIMILARITY.
FT	DISULFID	105	119	BY SIMILARITY.
FT	DISULFID	111	116	BY SIMILARITY.
FT	DISULFID	125	143	BY SIMILARITY.
FT	CARBOHYD	153	153	N-LINKED (GLUCNA...) (POTENTIAL).
FT	VARSPLIC	166	203	SCDKNLFVQKTSQTNNVIGLKSREALLAVIPVMWG --> RFKVPDASPAGSCHSRDGHPHHHFRGVSLVYKGGQETKG (in isoform II).
FT	VARSPLIC	204	289	/FTid=VSP 006474. Missing (in isoform II).
FT	VARSPLIC	187	216	/FTid=VSP 006475. GLKSRMRALIVIPVMGILLITIFGVFLYIK -> E (in isoform V).
FT	VARSPLIC	216	234	/FTid=VSP 006476. KKVKKPKDNEMLPFAAR -> SECSCGEEREGGFSPEPA S (in isoform III).
FT	VARSPLIC	235	289	/FTid=VSP 006477. Missing (in isoform III).
FT	VARSPLIC	216	222	/FTid=VSP 006478. KKVKKXP -> SQQETKG (in isoform IV).
FT	VARSPLIC	223	289	/FTid=VSP 006479. Missing (in isoform IV).
FT	VARSPLIC	223	289	/FTid=VSP 006480. Missing (in isoform IV).
FT	SEQUENCE	289 AA;	32111 MW;	C791CB6D2FEA574E CRC64;

Query Match	22.4%;	Score 256.5;	DB 1;	Length 289;	
Best Local Similarity	34.4%;	Pred. No. 2.3e-14;			
Matches 53;	Conservative	20;	Mismatches 72;	Indels 9;	Gaps 3

QY	41	SCKEDEYFVSGECCPKCSPGYRVKEACGELTGTVCBPCPGTIVIAHLNGLSKLOQCMCD 100
DB	25	TCSDKQYLHDGCCDLCQPGSLRTSHCTALEKTQCHPCDSGFSAQWNRIRCHQHRHCE 84
QY	101	PAMGLRASNCRSTENAVCGSPGHFCIVGDGHCACRAYATSSPGQVKGGTESQDT 160
DB	85	PNQGLRVKKEGTAESDVTCTCKEGHCTSKD---CRCAQHTPCIFGFGWMEATETDT 141
QY	161	LQNCPPGTFSPNGTL-EECQHTNWNPHMCEKK 193
DB	142	VCHPCPVGFSSNQSSLFEKC-----YPTWSCDK 170

RESULT 6				
CRMB VARV				
ID _CRMB VARV	STANDARD;	PRT;	349 AA.	
AC	P34015;	Q85407;	Q89098;	Q89118;
DT	01-FEB-1994	(Rel. 28,	Created)	
DT	01-FEB-1994	(Rel. 28,	Last sequence update)	
DT	28-FEB-2003	(Rel. 41,	Last annotation update)	
DE	Soluble TNF receptor II precursor (cytokine response modifying protein B).			
GN	CRMB OR G2R OR G4R.			
OS	Varola virus.			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
NCBI_Taxid=10255;				
[1]				
RN	SEQUENCE FROM N.A..			
RC	STRAIN=India-1367 / Isolate Ind3;			
EX	MEDLINE=9302281; PubMed=8384129;			
RA	Shchelkunov S N, Blinov V M, Sandakhchiev L S.;			
RT	"Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";			
RL	FEBS Lett. 319:80-83(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bangladesh-1975;			
RX	MEDLINE=94088747; PubMed=8264798;			
RA	Masung R.C., Esposito J.J., Liu L., Qi J., Utterback T.R.,			
RA	Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,			
RA	Selivanov N.A., Cavaliaro K.F., Kerlavage A.R., Many B.M.J.,			
RA	Venter C.J.;			

RESULT 6

[illegible]

CRMB_VARV	STANDARD:	PRT;
-----------	-----------	------

AC P34015; Q85407; Q89098; Q89118;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE
DE
SOLUBLE TNF RECEPTOR II PRECURSOR (CYTOSOLIC
P)

DE GN CRMB OR G2R OR G4R.

OS Variola virus.

OC viruses; dsDNA viruses, no RNA stage; Poxviridae; Poxvirinae; Chordopoxvirinae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=10255;

RN [I] CEOTENCE FROM N A
RD

SEQUENCE FROM N:1
STRATN=India-1967

RX MEDLINE=93202281; PubMed=8384129;

RA Shchelkunov S.N., Blinov V.M., Sa

RT "Genes of variola and vaccinia vi

RT protective mechanisms." ; 210-00-02 (1002)

RT
[3]
FEBS Lett. 319:80-83 (1993).

RN [2] SEQUENCE FROM N. A. PD

RC STRAIN=Bangladesh-1975;

RX MEDLINE=94088747; PubMed=8264798;

RA Massung R.F., Esposito J.J., Liu

RA Knight J.C., Aubin L., Yuran T.E.

RA Sellvanov N.A., Cavallaro K.F., N

RA VENTER C.O.;

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Syamane N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
[3]
SEQUENCE FROM N.A. (ISOFORM II).
MEDLINE=21117110; PubMed=1172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
"Regulation of CD40 function by its isoforms generated through alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
[4]
SEQUENCE FROM N.A. (ISOFORM I).
TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udgin T.B., Toshitsuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Richards S., McSwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.L., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
INTERACTION WITH TRAF3.
MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
[6]
INTERACTION WITH TRAF3.
MEDLINE=95129692; PubMed=7530216;
Sato T., Irie S., Reed J.C.;
"A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.";
FEBS Lett. 358:113-118(1995).
[7]
INTERACTION WITH TRAF3.
MEDLINE=98384149; PubMed=9718306;
Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J., Kehry M.R.;
"CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-oligomerization.";
Biochemistry 37:11836-11845(1998).
[8]
INTERACTION WITH TRAF5.
MEDLINE=98172745; PubMed=9511754;
Mizushima S.-I., Fujita M., Ichida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.;
"Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5).";
Gene 207:135-140(1998).
[9]
INTERACTION WITH TRAF6.
MEDLINE=98095703; PubMed=9432981;
Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K., Okumura K., Yamamoto T., Nagaoka H., Takemori R.;
"Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates extracellular signal-regulated kinase (ERK) activity in CD40 signaling along a ras-independent pathway.";
J. Exp. Med. 187:237-244(1998).
[10]
3D-STRUCTURE MODELING OF 24-144.
RP MEDLINE=97189482; PubMed=9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
Proteins 27:59-70(1997).
[11]
3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RP MEDLINE=98266353; PubMed=9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
[12]
X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH TRAF3.
RP MEDLINE=20442386; PubMed=10984535;
Ni C.Z., Welsh K., Leo E., Chieu C.K., Wu H., Reed J.C., Ely K.R.;
"Molecular basis for CD40 signaling mediated by TRAF3.";
Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
[13]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH TRAF3.
RP MEDLINE=22000222; PubMed=12005438;
Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C., Satterthwait A.C., Cheng G., Ely K.R.;
"Downstream regulator TANK binds to the CD40 recognition site on TRAF3.";
Structure 10:403-411(2002).
[14]
VARIANT HIGM3 ARG-83.
RP MEDLINE=21532985; PubMed=11675497;
Ferrari S., Giliani S., Insalaco A., Al-Chonaim A., Scorsina A.R., Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G., Levy I., Cacialan N., Durandy A., Tbakhi A., Notarangelo L.D., Plebani A.;
"Mutations of CD40 gene cause an autosomal recessive form of immunodeficiency with hyper IgM.";
Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I); secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP 006472, VSP 006473;
CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC -!- DISEASE: Defects in TNFSF5 are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:608943]. HIGM3 is an autosomal recessive disorder which includes an inability of B cells to undergo isotype switching, one of the final differentiation steps in the humoral immune system, an inability to mount an antibody-specific immune response, and a lack of germinal center formation.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.rcbi.nlm.nih.gov/prow/cd/cd40.htm".

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EMBL; X50592; CAA43045.1; -
EMBL; AL035662; CAC17670.1; -
EMBL; AJ300189; CAC29424.1; -
EMBL; BC012419; AAI12419.1; -
FIR; S04460; A60771.
PDB; 1CDF; 01-APR-97.
PDB; 1PLL; 18-OCT-00.
PDB; 1LOA; 08-FEB-00.
PDB; 1CZ2; 26-SEP-01.

Query Match 22.2%; Score 254; DB 1; Length 277;
Best Local Similarity 31.1%; Pred. No. 3.6e-14;
Matches 56; Conservative 30; Mismatches 78; Indels 16; Gaps 5;
20 VLRLVLYLTLFLGAPCVAPAL-----PSCKEDYVPGSECCPKCPGVRVKEACGELGTG 74
1 MVLPLQCVLWG--CLLTAVHPPTACREKQYLINSQCCLCPGGKLVSDCTFTETE 58
75 CBPCPPGTIAHLNGLSKLQCCMDPAMGLRASRNCSTENAVCGSPGHFCIVQGDH 134
59 CLPCGSEFLDTWNRETHCHQHKYCDPLGLRVQKQGTSETDTICTCEGWHC---TSEA 115
135 CAACRAYATSSQQRVQKGGTSQTLQCNCPPTFS--PNTLEECQHTQWPNHMEKK 193
116 CBSVLHRSCTPGFGVQKQIATGVSDTICEPCVGFNSVSAFEKCHPWTG-----CETK 170

ULT 8
MB_COMPX
O73559; P87602; PRT; 351 AA.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein B).
(CRMB1 OR D2L) AND (CRMB2 OR I4R).
Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10243;
[1]
SEQUENCE FROM N.A.
STRAIN=GRI-90 / Grishak;
MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
Ryzankina O.I., Gutorov V.V., Kotwal G.J.;
"The genomic sequence analysis of the left and right species-specific
terminal region of a cowpox virus strain reveals unique sequences and
a cluster of intact ORFs for immunomodulatory and host range
proteins";
Virology 243:432-450(1998).
[2]
FUNCTION.
STRAIN=Brighton red;
MEDLINE=94378510; PubMed=8091665;
Hu P.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor";
Virology 204:343-356(1994).
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
the modification of TNF-mediated antiviral processes.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.

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EMBL; X94355; CAA64087.2; -
DR EMBL; X94355; CAD90756.1; -
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 351
FT REPEAT 21 67
FT REPEAT 31 67
FT REPEAT 69 110
FT REPEAT 99 110
FT DISULFID 32 43
FT DISULFID 44 57
FT DISULFID 47 67
FT DISULFID 70 85
FT DISULFID 88 102
FT DISULFID 92 110
FT CARBOHYD 103 103
FT CARBOHYD 191 191
FT CARBOHYD 250 250
SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EF4ESD7C7 CRC64;

Query Match 21.2%; Score 243.5; DB 1; Length 351;
Best Local Similarity 31.0%; Pred. No. 3.3e-13;
Matches 54; Conservative 27; Mismatches 76; Indels 17; Gaps 6;
21 LRLVLYLTLFLGAPC-----YAPALPSCKEDYVPGSECCPKCPGVRVKEACGEL 70
1 MKSVLYSVTLFLSCIINGRDIAPHAPNGKCKDNEVNRHNLCLSCPPTGYASRLCDCK 60
71 --TGTVCPECPGTIAHLNGLSKLQCC-MCDPAMGLRASRNCSTENAVCGSPGHFC 127
61 TMTNTQCTPCGGSTFTSRNNHLPACLSCNGRCD--SNQVTRSCNTHNRICECAPGYVC 118
128 IVQGDGHCAACRAYATSSPGQVRVQKGGTSQTLQCNCPPTFSN-GTLEECQ 180
119 LLKSGSGCKACVSKQKIGYGV-SGHTSTGTVGVCSGCLGTYSHTVSSADKCE 171

RESULT 9
ID TNRS_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (P-fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
cattle";
RT Immunology 90:294-300(1997).
RL CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
similarity).

!- SUBCELLULAR LOCATION: Type I membrane protein.
!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL: U57745; AAC48710.1; --
HSSP: P25942; 1CDF.
InterPro: IPR008063; Fas_receptor.
Pfam: PF001368; TNFR_c6.
PRINTS: PF002020; TNFR_C6; 4.
SMART: SM00208; FASRECEPTOR.
PROSITE: PS00652; TNFR_NGFR_1; 1.
PROSITE: PS00500; TNFR_NGFR_2; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL 1 19
CHAIN 20 >269
TUMOR NECROSIS FACTOR RECEPTOR
SUPRACELLULAR (POTENTIAL).
DOMAIN 20 193
TRANSMEM 194 215
DOMAIN 216 >269
REPEAT 25 60
REPEAT 61 103
REPEAT 104 144
REPEAT 145 187
REPEAT 188 215
DISULFID 26 37
DISULFID 38 51
DISULFID 41 59
DISULFID 62 77
DISULFID 83 103
DISULFID 105 119
DISULFID 111 116
DISULFID 125 143
CARBOHYD 153 153
CARBOHYD 180 180
NON_TER 269 269
SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;
Query Match 21.1%; Score 242; DB 1; Length 269;
Best Local Similarity 29.8%; Pred No. 3.4e-13;
Matches 53; Conservative 32; Mismatches 31; Indels 12; Gaps 4;
20 VRLVLYLTLFLG---APCYALPSCKEDEYVSGECPCSPGYRVKEACGELTGTVCE 76
1 MVRFLQLFLWGFLLTAVHSEFATACGEKQYVNSLCCDLCPGQKLVNDCTEVSKTEQC 60
77 PCPPCTYIAHLNGLSKLCCQMCOPMGLSRNCRSTENAVGCSFGHFCIVQDGDHCA 136
61 SCGKGFLSTWNRKYCHEHYCPNGLRQSGTLNTDTICVCEGQC---TSHTC 117
137 ACRAVATSPGQVKGGTESQDLCQCPPTGTS-PNGTLEECQHOTNPWPMCEK 193
118 SCTPHSLCLPGGVKQIATGLDITVCEPCPLGFTSNVSSAFCKHRWTS-----CERK 170
STANDARD; PRT; 435 AA.

RESULT 10
TNF3 HUMAN
P36941;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 3 precursor
(lymphotoxin-beta receptor) (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor C receptor).
LTR OR TNFRSF3 OR TNFR.
Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RX Baers M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
transcribed sequences derived from a somatic cell hybrid";
RL Genomics 16:214-218(1993).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RX Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor";
RL Science 264:707-710(1994).
RN [4]
RN CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006;
RX Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
death in HeLa cells";
RL J. Biol. Chem. 274:11868-11873(1999).
RN [5]
RN FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RX Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
LIGHT-mediated apoptosis of tumor cells";
RL J. Biol. Chem. 275:14307-14315(2000).
RN [6]
RN INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299;
RX Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF3, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor";
RL J. Biol. Chem. 271:14661-14664(1996).
RN [7]
RN INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RX Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA Gascoyne R.D., Berem K., McFadden D., Shabalik A., Hugh J.,
RA Reynolds A., Cleveland C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
adult, fetal, and tumor tissues";

```

57 ICSSRPPGPTYYSKCSRIRDVTVCATCAENSYNHEWNYLTICQLCRPCDPVMGLEIAPC 116
112 SRTENAVCGCSPGHFC-----IVQGDHCAACRA--Y 141
117 TSKEKTCRCQCGMFCAAWALBCTHCELLSDPCPTEAELKDEVGKNNHCVPCKAGHFQ 176
142 ATSPGQRVQ-----KGTSSQTLQN---CPP---CT----- 169
177 NTSPSARCQPHTRCENQGLVEAPGTAQSDTCKNPLEPLPPEMSGTMLMLAVLPLAF 236
170 FSPNGTLEECQHOTWPNH--MCEK 192
237 FLLAIVFSC---IWKSHPSLCRK 257

RESULT 11
VT2_MXVL
ID ID VT2_MXVL STANDARD; PRT; 326 AA.
P29825;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor soluble receptor precursor (Protein T2).
M002L OR T2.
MXVMA virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Leptopoxvirus
NCBI_TaxID=31530;
[1]
SEQUENCE FROM N.A.
MEDLINE=91335768; PubMed=1651597;
Upton C., Macen J.L., Schreiber M., McFadden G.;
"Myxoma virus expresses a secreted protein with homology to the tumor
necrosis factor receptor gene family that contributes to viral
virulence.";
Virology 184:370-382(1991).
[2]
SEQUENCE FROM N.A.
MEDLINE=20032073; PubMed=10562494;
Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
Macaulay C., Waller D., Evans D., McFadden G.;
"The complete DNA sequence of myxoma virus.";
Virology 264:298-318(1999).
-1- REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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EMBL; M95181; AAA46632.1; -
EMBL; AF170726; AAF15046.1; -
EMBL; AF170726; AAF14887.1; -
EMBL; A23729; CAA01688.1; -
PIR; A40566; GOVZML.
HSSP; P19438; INCF.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Glycoprotein; Repeat; signal.
SIGNAL 1 16 POTENTIAL.
CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
REPEAT 27 62 TNFR-CYS 1.
REPEAT 63 104 TNFR-CYS 2.
REPEAT 105 147 TNFR-CYS 3.

```


MEDLINE=99253915; PubMed=10318773;
 Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 "A newly identified member of tumor necrosis factor receptor
 superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 J. Biol. Chem. 274:13733-13736(1999).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Lung;
 MEDLINE=20122600; PubMed=10655513;
 Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,
 Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
 independent of gene amplification and its location in a four-gene
 cluster";
 Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 [4]
 SEQUENCE FROM N.A.
 Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 TISSUE=Lung and Skin;
 MEDLINE=22388257; PubMed=12477932;
 Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udell T.B., Toshiyuki S., Carlincl P., Frange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S., Krzywinski M.I., Skalska U., Smalusz D.E.,
 Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 -1- SUBCELLULAR LOCATION: Secreted.
 -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 Detected in adult stomach, spinal cord, lymph node, trachea,
 spleen, colon and lung. Highly expressed in several primary tumors
 from colon, stomach, rectum, esophagus and in SW480 colon
 carcinoma cells.
 -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 or send an email to license@isb-sib.ch).

 EMBL; AF104419; RAD03056.1; -
 EMBL; AF134240; RAD2688.1; -
 EMBL; AF217796; AAF3244.1; -
 EMBL; AF217793; AAF33685.1; -
 EMBL; AF217794; AAF33686.1; -
 EMBL; AL121845; CAC03668.1; -
 EMBL; BC017065; AAH17065.1; -
 EMBL; BC034349; AAH34349.1; -
 HSP; OA4763; IDOG; TNFRSF6B.
 Genew; HGNC:111921; TNFRSF6B.
 MIM; 603361; -
 GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR
 SUPERFAMILY MEMBER 6B.
 FT REPEAT 31 70
 FT REPEAT 72 113 TNFR-CYS 1.
 FT REPEAT 115 150 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 196 235 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
 Query Match 20.2%; Score 231; DB 1; Length 300;
 Best Local Similarity 35.8%; Pred. No. 3.1e-12;
 Matches 64; Conservative 15; Mismatches 78; Indels 22; Gaps 8;
 QY 16 PRTDVLRLVLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSGPGYRKEACG 68
 DB 7 PGLSLLCLVLPAL---LPVAVRGVAETPTPRDAETGERLVCAQCPGTFVQPC 63
 QY 69 ELTGVTCPPPGTGVIAHLNGLSKCLQCMCDPAMGLR--ASRNCSTENAVCCSPGHF 126
 DB 64 RDSPTTCGCPPHRYTQFWNYLER---CRYCNVLCGEREEARACHATHNACRCRTGFF 120
 QY 127 CIVQGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQHTN 184
 DB 121 A-----HAGFCLERHASCPPGAGVIAPGTPSQNTCCQCPPTFSASSSSEQCQPHRN 173
 RESULT 14
 TR16 MOUSE
 ID TR16 MOUSE STANDARD; PRT; 417 AA.
 AC Q920F1;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 affinity nerve growth factor receptor) (NGF receptor) (Low affinity
 neurotrophin receptor p75NTR).
 DE NGFR OR TNFRSF16.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=A.
 RX MEDLINE=99077793; PubMed=9857182;
 RA Tuiffereau C., Benejean J., Blondel D., Kieffer B., Flamand A.;
 "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
 receptor for rabies virus";
 EMBO J. 17:7250-7259(1998).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 AND NT-4. Can mediate cell survival as well as cell death of
 neural cells (By similarity). Binds to rabies virus glycoprotein
 Gs.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-

Pfam; PF00020; TNFR_C6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00650; TNFR_NGFR_2; 3.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL 1 30 POTENTIAL
CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR

DOMAIN 31 223 SUPERFAMILY MEMBER 3.
TRANSMEM 224 244 EXTRACELLULAR (POTENTIAL).
DOMAIN 245 415 POTENTIAL.
REPEAT 42 81 CYTOPLASMIC (POTENTIAL).
REPEAT 82 124 TNFR-CYS 1.
REPEAT 125 170 TNFR-CYS 2.
REPEAT 171 213 TNFR-CYS 3.
DISULFID 43 58 TNFR-CYS 4.
DISULFID 59 72 BY SIMILARITY.
DISULFID 62 80 BY SIMILARITY.
DISULFID 83 98 BY SIMILARITY.
DISULFID 101 116 BY SIMILARITY.
DISULFID 104 124 BY SIMILARITY.
DISULFID 126 132 BY SIMILARITY.
DISULFID 139 150 BY SIMILARITY.
DISULFID 142 169 BY SIMILARITY.
DISULFID 172 187 BY SIMILARITY.
CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 415 AA; 44956 MW; 298326A566AEF661 CRC64;

Query Match 18.9%; Score 217; DB 1; Length 415;
est Local Similarity 27.5%; Pred. No. 6e-11;
atches 60; Conservative 19; Mismatches 69; Indels 70; Gaps 10;

7 WGP-----PWRSTPTDVLRLVLTFLGAPCYAPALPSCKEDEY-- 47
14 WGPLLLGLSLVASQPLVPPYRIENOT-----CWD-----QDKYEY 52
48 PVGSECCPKCSFGYKACGELTGTVCPCPGPTTYIAHLNGLSKLCQCMCDPAMGLRA 107
53 PMHDVCCSRCPGGEFVFAVCSSQDTVCKTCHNSYNEHNNHLSLTCOLCRPCDIVLGFE 112
108 SRNCSRTENAVCGCSFGHFCIVQGD--HCAACRAYATSSPGQVQKGTESQ----- 158
113 VAFCTSDRKAECRCQFGMSCVYLDNECVHCEERLV-----LCQFGTBAEVTDEIMD 164
159 -DTLQCNCPPTGTF-----SPNGTLECCQHTNPNMHCE 191
165 TDVNCVPCXPGHFGNTSSPRA---RCQ-----PHTRC 194

Arch completed: June 10, 2004, 12:32:27
Time: 39 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: June 10, 2004, 12:02:03 ; Search time 80 Seconds
(without alignments)
776.964 Million cell updates/sec

le: US-09-934-289A-18

fect score: 1146
quence: 1 MBPPGDWGPWRPRTDV.....BCQHTNPNHMCCKKAKG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1017041 segs, 315518202 residues

tal number of hits satisfying chosen parameters: 1017041

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query %	Match	Length	DB ID	Description
1	920.5	80.3	283	6	Q9XSZ8	Q9xs28 cercopithec
2	552	48.2	273	11	Q8W0M9	Q8w0m9 mus musculu
3	460	40.1	199	4	Q8N634	Q8n634 homo sapien
4	323	28.2	196	11	Q8VC17	Q8vc17 mus musculu
5	292	25.5	278	6	Q8SQ34	Q8sq34 sus scrofa
6	272	23.7	483	13	Q800K7	Q800k7 paralichthy
7	270.5	23.6	348	12	Q800K7	Q800k7 monkeypox v
8	270.5	23.6	348	12	O57277	O57277 monkeypox v
9	270.5	23.6	349	12	O57100	O57100 monkeypox v
10	268.5	23.4	349	12	O57101	O57101 monkeypox v
11	268.5	23.4	349	12	O57102	O57102 monkeypox v
12	268.5	23.4	349	12	O57291	O57291 monkeypox v
13	266.5	23.3	348	12	O57103	O57103 monkeypox v
14	266.5	23.3	349	12	O57098	O57098 camelipox vi
15	266.5	23.3	349	12	O57284	O57284 camelipox vi
16	264.5	23.1	349	12	O57099	O57099 monkeypox v

17	263.5	23.0	462	13	Q805B0	Q805b0 gallus gall
18	262.5	22.9	349	12	O57097	O57097 camelipox vi
19	258.5	22.6	289	11	Q8K2X6	Q8k2x6 mus musculu
20	257.5	22.5	351	12	O57117	O57117 cowpox viru
21	255.5	22.3	169	11	Q9JKE0	Q9jke0 rattus norv
22	255	22.3	348	12	O57112	O57112 variola vir
23	254	22.2	223	4	Q86YK5	Q86yk5 homo sapien
24	254	22.2	349	12	O57111	O57111 variola vir
25	254	22.2	349	12	O57110	O57110 variola vir
26	254	22.2	349	12	O80SR3	O80sr3 variola vir
27	246.5	21.5	349	12	O57109	O57109 variola vir
28	239	20.9	350	12	O57116	O57116 cowpox viru
29	238	20.8	277	6	Q8WMQ2	Q8wmq2 ovis aries
30	236.5	20.6	351	12	O57121	O57121 cowpox viru
31	235	20.5	171	12	Q7TFH9	Q7tfh9 rhesus cyto
32	232.5	20.3	349	12	O57305	O57305 cowpox viru
33	229.5	20.0	326	12	O57122	O57122 cowpox viru
34	229	20.0	347	12	O57119	O57119 cowpox viru
35	228.5	19.9	326	12	O57120	O57120 cowpox viru
36	228	19.9	360	12	O57118	O57118 cowpox viru
37	227	19.8	285	13	Q9DGH7	Q9dgh7 gallus gall
38	227	19.8	318	13	Q7T2H3	Q7t2h3 oncorhynch
39	226.5	19.8	350	12	O57123	O57123 cowpox viru
40	225.5	19.7	274	6	Q7YRL5	Q7yrl5 canis fami
41	225.5	19.7	347	12	O57115	O57115 cowpox viru
42	225.5	19.7	355	12	O85308	O85308 cowpox viru
43	219.5	19.2	312	13	Q9DGH8	Q9dgh8 gallus gall
44	219.5	19.2	467	13	Q80010	Q80010 gallus gall
45	218.5	19.1	267	6	O02764	O02764 oryctolagus

ALIGNMENTS

RESULT 1

Q9XSZ8	PRELIMINARY;	PRT;	283 AA.
ID	O9XSZ8		
AC	O9XSZ8;		
DT	01-NOV-1999 (TrEMBLrel. 12, Created)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	HveAs.		
GN	HVEAS.		
OC	Cercopithecus aethiops (Green monkey) (Grivet).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC	Cercopithecinae; Cercopithecus.		
OX	NCBI_TaxID=9534;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RX	MEDLINE=99296730; PubMed=10366573;		
RA	Foster T.P., Chouljenko V.N., Kousculas K.G.;		
RT	"Functional characterization of the HveA homolog specified by African		
RT	green monkey kidney cells with a herpes simplex virus expressing the		
RL	green fluorescence protein.";		
RL	Virology 258:365-374(1999).		
DR	EMBL; AF147720; AAD37381.1; -		
DR	HSP; Q92956; 1JMA		
DR	GO; GO:0016020; C.membrane; IEA.		
DR	GO; GO:0004888; F.transmembrane receptor activity; IEA.		
DR	GO; GO:0006915; P.apoptosis; IEA.		
DR	GO; GO:0006955; P.immune response; IEA.		
DR	GO; GO:0007165; P.signal transduction; IEA.		
DR	InterPro; IPR008063; Fas receptor.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00020; TNFR_c6; 3.		
DR	PRINTS; PR01680; FASRECEPTOR.		
DR	SMART; SMO0208; TNFR; 3.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.		
DR	PROSITE; PS00652; TNFR_NGFR_2; 2.		
DR	PROSITE; PS00652; TNFR_NGFR_2; 2.		
DR	SEQUENCE 283 AA; 30199 MW; 397951C6617FB3AA CRC64;		
DR	SEQUENCE 283 AA; 30199 MW; 397951C6617FB3AA CRC64;		

Query Match 80.3%; Score 920.5; DB 6; Length 283;
Best Local Similarity 82.3%; Pred. No. 8.6e-88;
Matches 158; Conservative 9; Mismatches 20; Indels 5; Gaps 1;

1 MEPPDGMGPPWRSTPRDVLRLVLYTLFLGAPYAPALPSCCKEDYFVGSCECCPKCSPG 60
1 MEPPDGMGPPWRSTPRDVLRLVLYTLFLGSSCYAPALPSCCKEDYFVGSCECCPKCSPG 60
61 YRVKEACGLTGTVCBPPGTYIAHLNGLSKLQCCQMDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGLTGTVCBPPGTYIAHLNGLSKLQCCQMDPAMGLRASRNCSTENAVCG 120
61 PHVQACGEQTGTVCBPPGTYIAHLNGLSKLQCCQMDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGKGTESQDTLQCNCPPTGFSNGTLEECQ 180
121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGKGTESQDTLQCNCPPTGFSNGTLEECQ 180
181 HQTWPNHMCXK 192
181 H-----GNKCSK 187

RESULT 2
10WMS
Q80WM9 PRELIMINARY; PRT; 275 AA.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Thymus;
Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
"Light regulation in a murine model of ovarian carcinoma";
Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY264405; AA089081.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; P:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; F: Fas receptor.
Pfam; PF00020; TNFR_c6; 4-
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00050; TNFR_NGFR_2; 3.
V Receptor; Signal.
SIGNAL 1 38 Potential.
SEQUENCE 275 AA; 30171 MW; C4A7EAD8FEC0521D CRC64;

Query Match 48.2%; Score 552; DB 11; Length 275;
Best Local Similarity 53.3%; Pred. No. 2.1e-49;
Matches 98; Conservative 18; Mismatches 68; Indels 0; Gaps 0;

1 MEPPDGMGPPWRSTPRDVLRLVLYTLFLGAPYAPALPSCCKEDYFVGSCECCPKCSPG 60
1 MEPLFCGWSAPMSQAFDTNTFLVPCVFLNLLQRIASQPSRCRFEFLVGECCPMCNPG 60
61 YRVKEACGLTGTVCBPPGTYIAHLNGLSKLQCCQMDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGLTGTVCBPPGTYIAHLNGLSKLQCCQMDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGKGTESQDTLQCNCPPTGFSNGTLEECQ 180
121 CIPGYECENQDGSHTCLQHTTCPPGQVKEKRGTHDQTVACDLTGTSLSGTQECL 180
181 HQTWPNHMCXK 192

Db 181 PWTN 184

RESULT 3
Q8N634 PRELIMINARY; PRT; 199 AA.
Q8N634
AC Q8N634; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029848; AAH29848.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6; 1.
DR Pfam; PF00020; TNFR_c6; 1.
KW Receptor.
SQ SEQUENCE 199 AA; 21404 MW; F04A2264BC16D00A CRC64;

Query Match 40.1%; Score 460; DB 4; Length 199;
Best Local Similarity 95.4%; Pred. No. 5.9e-40;
Matches 83; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 101 PAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQVKGKGTESQDT 160
17 PAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQVKGKGTESQDT 76
QY 161 LCQNCPPGTSPNGTLEECQHQT--NW 195
17 LCQNCPPGTSPNGTLEECQHQT--NW 103

RESULT 4
Q8VC17 PRELIMINARY; PRT; 196 AA.
Q8VC17
DT 01-NAR-2002 (TrEMBLrel. 20, Created)
DT 01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022125; AAH22125.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; F: Fas receptor.
DR InterPro; IPR001368; TNFR_c6; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Hypothetical protein.
NON_TER 1

SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260B8 CRC64;
 Query Match 28.2%; Score 323; DB 11; Length 196;
 est Local Similarity 56.3%; Pred. No. 1.1e-25;
 atches 58; Conservative 10; Mismatches 35; Indels 0; Gaps 0;
 82 TYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCGSPGHFCIVODGDHCAACRAY 141
 2 TYTANGLSKLCQCMCDPAMGLRASNCRSTENAVCGSPGHFCIVODGDHCAACRAY 61
 142 ATSSPGQVQKGTESQDTLCQCPPTFTS-PNGTLEECOHQTN 184
 62 TTCPSQVQKGTESQDTLCQCPPTFTS-PNGTLEECOHQTN 104
 ULT 5
 Q34 PRELIMINARY; PRT; 278 AA.
 Q8S034;
 01-JUN-2002 (Tremblrel. 21, Created)
 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 CD40.
 Sus scrofa (Pig).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 [1]
 SEQUENCE FROM N.A.
 West K.A., Li A.W., Rowden G.;
 "Characterization of the Porcine CD40 Molecule."
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 EMBL; AF248545; AAL92924.1;
 GO; GO:0015020; C:membrane; IEA.
 GO; GO:0004888; F:transmembrane receptor activity; IEA.
 GO; GO:0006915; P:apoptosis; IEA.
 GO; GO:0006955; P:immune response; IEA.
 GO; GO:0007165; P:signal transduction; IEA.
 InterPro; IPR008063; Fas receptor.
 InterPro; IPR001368; TNFR_c6.
 Pfam; PF00020; TNFR_c6; 4.
 PRINTS; PR01680; FASRECEPTOR.
 SMART; SM00208; TNFR; 4.
 PROSITE; PS00652; TNFR_NGFR_1; 1.
 PROSITE; PS00050; TNFR_NGFR_2; 4.
 SEQUENCE 278 AA; 30951 MW; 20D446E44AF93DD2 CRC64;
 Query Match 25.5%; Score 292; DB 6; Length 278;
 est Local Similarity 36.2%; Pred. No. 2.7e-22;
 atches 63; Conservative 25; Mismatches 76; Indels 10; Gaps 4;
 21 LRLVLYLFLGAPCVAPALPSCKEDEYVGVSECCPKSPGVRVKEAGELTGTVCPCPP 80
 6 LKCLLWGFLTAHVHEPP-TCKENQFTNSCCNLCPFGKLVNHTVETETECPLCSS 64
 81 GYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCGSPGHFCIVODGDHCAACRA 140
 65 SEFLATWNRKHCHQKCDNLGLQVREGTSKTDITCVCSGHHG---TNSACESCTL 121
 141 YATSSPGQVQKGTESQDTLCQCPPTFTS-PNGTLEECOHQTNWNNHCEKK 193
 122 HSLCPFLGLVKQMATEVSDTICEPCPVGFNFNSASEKQCPWTS-----CESK 170
 ULT 6
 OK7 PRELIMINARY; PRT; 483 AA.
 Q800K7;
 01-JUN-2003 (Tremblrel. 24, Created)
 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 Tumor necrosis factor receptor-2.
 TNFR-2.

OS Paralichthys olivaceus (Flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectoidei; Paralichthyidae; Paralichthys.
 OX NCBI_TaxID=8255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park C., Kurobe T., Hirono I., Aoki T.;
 RT "Cloning and characterization of cdnas for two distinct tumor necrosis
 RT factor receptor superfamily genes from Japanese flounder Paralichthys
 RT olivaceus."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB080947; BAC65226.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6;
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 3.
 KW Receptor.
 SQ SEQUENCE 483 AA; 52227 MW; BE55874A8C7F2085 CRC64;
 Query Match 23.7%; Score 272; DB 13; Length 483;
 Best Local Similarity 36.9%; Pred. No. 5.8e-20;
 Matches 52; Conservative 18; Mismatches 69; Indels 2; Gaps 2;
 QY 46 EYVGVSECCPKSPGVRVKEAGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGL 105
 DB 33 EYREQDLCKCKPFGQLIKQCSATESVCKQDSGQYMEKYNIAQKLSCKNCKNKG 92
 QY 106 RASRNCSTENAVCGSPGHFCIVQ-DGDHCAACRAYATSSPGQVQKGTESQDTLCQ 164
 DB 93 QYACQCSSTFTGCVCKPKGMYCIMDFNPYCAECNYSQCRAGVGLPKGANSVDVKCEL 152
 QY 165 CPPGTFS-PNGTLEECOHQTN 184
 DB 153 CPDGMFNTSNTETCRPTD 173
 RESULT 7
 OS7108 PRELIMINARY; PRT; 348 AA.
 ID OS7108;
 AC OS7108;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 GN CRMP.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Zaire-1970;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88142; AA594367.1;
 DR HSP; Q92856; LUMA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6;
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KW Receptor.
 SQ SEQUENCE 348 AA; 38212 MW; BE55979057DEC91P CRC64;
 Query Match 23.6%; Score 270.5; DB 12; Length 348;
 Best Local Similarity 32.4%; Pred. No. 5.9e-20;

Matches 57; Conservative 26; Mismatches 78; Indels 15; Gaps 5

21 LRVLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPKSPGYRVKEACGEL 70
1 MRSVLVSYLFLFSLCIINGRDIAHPASNGKCKDNEYRNRNLCCLSCPPTGYASRLCDISK 60
71 TGTVCPECPGGYIAHLNGLSKLCLOQC-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
61 TNTQCTFGSDTFTSHNHLQALSCNGRCD--SNQVETKSCNTTHNRICECSPTGYICLL 118
130 QGDHCHCAACRAYATSPGQRVKGSTESQDTLQCNCPPTGTFSPN-GLTEECQOHTN 184
119 KGSSGCRCTCISKTKGIGVGV-SGYTSTGVDVICSPGPGTYSHTVSTSDKCEPVT 173

RESULT 8

057277 PRELIMINARY; PRT: 348 AA.
057277;
01-JUN-1998 (TEMBLrel. 06, Created)
01-JUN-1998 (TEMBLrel. 06, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
Tumor necrosis factor receptor II homolog (J2R) (J2L).
CRMB OR J2R OR J2L.
Monkeypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10244;
[1]
SEQUENCE FROM N.A.
STRAIN=ZAIRE-1996 /96-17, and ZAIRE-1996 /96-16;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=ZAIRE-96-I-16;
MEDLINE=21592287; PubMed=11734207;
Shchelkunov S.N., Tolmenin A.V., Babkin I.V., Safronov P.F.,
Ryzhankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
Mikhaev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
Sandakchiev L.S.;
"Human monkeypox and smallpox viruses: genomic comparison."
FEBS Lett. 509:66-70(2001).
[3]
SEQUENCE FROM N.A.
STRAIN=ZAIRE-96-I-16;
Shchelkunov S.N., Tolmenin A.V., Safronov P.F., Gutorov V.V.,
Ryzhankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakchiev L.S.;
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
EMBL: U88543; AAB94378.1; -;
EMBL: U87841; AAB94358.1; -;
EMBL: AF380138; AAL40648.1; -;
EMBL: AF380138; AAL40460.1; -;
HSP; Q92956; IJMA.
GO: G0:0004872; F:receptor activity; IEA.
InterPro: IPR001368; TNFR_c6.
pfam: PF00020; TNFR_c6; 2.
SMART: SM00208; TNFR; 2.
PROSITE: PS00652; TNFR_NGFR_1; 2.
PROSITE: PS00050; TNFR_NGFR_2; 2.
SEQUENCE 348 AA; 36212 MW; 540195215562D8F CRC64;

Query Match 23.6%; Score 270.5; DB 12; Length 348;
Best Local Similarity 32.4%; Pred. No. 5.9e-20;
Matches 57; Conservative 26; Mismatches 78; Indels 15; Gaps 5;

21 LRVLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPKSPGYRVKEACGEL 70
1 MRSVLVSYLFLFSLCIINGRDIAHPASNGKCKDNEYRNRNLCCLSCPPTGYASRLCDISK 60
71 TGTVCPECPGGYIAHLNGLSKLCLOQC-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129

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Db      61  TWTQCTPGSGDTTFSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRIKICSPGYCYLL 118
QY      130  QDGHCAACRAYATSPGQRVQKGTTESODTLQCNCPPGTFSPN- GTLEBCQHQTN 184
      :      :      :      :      :      :      :      :      :      :
Db      119  KGSSGCRTCISKTKCGIGYGV- SGYTSTGDVICSPCGPGTYSHTVSTDKCEPVT 173

RESULT 9
OS7100 PRELIMINARY; PRT; 349 AA.
ID      057100
AC      057100;
DT      01-JUN-1998 (TrEMBLrel. 06, Created)
DT      01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Tumor necrosis factor receptor II homolog.
DN      CMB.
OS      Monkeypox virus.
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Orthopoxvirus.
OC      NCBI_TaxID=10244;
RN      [1]
RX      SEQUENCE FROM N.A.
RP      STRAIN=Nigeria-1971;
RA      Loparev V.N., Parsons J.M., Esposito J.J.;
RT      "DNA sequence analysis as a criterion for allocation of the
RT      orthopoxviruses to a particular species.";
RL      Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U87844; AAB94361.1; -.
DR      HSSP; Q92956; LUMA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      InterPro; IPR001368; TNFR_c6.
DR      Pfam; PF00020; TNFR_C6; 2.
DR      SMART; SM00208; TNFR; 2.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
DR      PROSITE; PS50050; TNFR_NGFR_2; 2.
KW      Receptor.
KW      Receptor.
SQ      SEQUENCE 349 AA; 38239 MW; DF6C280D478F2422 CRC64;

Query Match      23.6%; Score 270.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 5,9e-20;
Matches 56; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY      21  LRLVLYTLGLAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
      :      :      :      :      :      :      :      :      :      :
Db      1  MRSVLVSYILFLSCIITINGRIADPHAPAGKCKDEYRSNLCCLSCPPGTYASRLCDSK 60

QY      71  TGTVCPCPPGTYYIAHLNGLSKLQCC-NCDFAMGLRASRNCRTENAVCCGSPGHFV 129
      :      :      :      :      :      :      :      :      :      :
Db      61  TWTQCTPGSGDTTFSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRIKICSPGYCYLL 118

QY      130  QDGHCAACRAYATSPGQRVQKGTTESODTLQCNCPPGTFSPN- GTLEBCQ 180
      :      :      :      :      :      :      :      :      :      :
Db      119  KGASGCSCTISKTKCGIGYGV- SGYTSTGDVICSPCGPGTYSHTVSTDKCE 169

RESULT 10
OS7101 PRELIMINARY; PRT; 349 AA.
ID      057101
AC      057101;
DT      01-JUN-1998 (TrEMBLrel. 06, Created)
DT      01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Tumor necrosis factor receptor II homolog.
DN      CMB.
OS      Monkeypox virus.
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Orthopoxvirus.
OC      NCBI_TaxID=10244;
RN      [1]
RX      SEQUENCE FROM N.A.
RP      STRAIN=Zaire-1977;
RA      Loparev V.N., Parsons J.M., Esposito J.J.;
RT      "DNA sequence analysis as a criterion for allocation of the

```


Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

EMBL; U87847; AAB94364.1; -;
HSP; Q92956; 1JMA.
GO: GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor.
SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 23.3%; Score 266.5; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 56; Conservative 26; Mismatches 79; Indels 15; Gaps 5;
21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVSGECPCPKSGYRVKEACGEL 70
1 MESALYSYILFLSCIIINGRDVTPYAPSGKCKNEYKRNLCCLSCPPGTYSARLDCSK 60
71 TGTVCPCPCPGTYIAHLNGLSKLQCC-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
61 TNTQCTPCGSGTFTSRNNHLPACLSNCRCD--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDGHCAACRAYATSSPGQVKGGTESQDTLCQCPPTGTFSPN-GTLEECQ 180
119 KGSSGCKACVSTKCGIGYGV-SGHTSAGDVICSPCGLTGTYRTVSSADKCE 169

RESULT 14
57098
D 057098 PRELIMINARY; PRT; 349 AA.

01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Tumor necrosis factor receptor II homolog.
CRMB.
Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=203174;
SEQUENCE FROM N.A.
Loparev V.N., Parsons J.M., Esposito J.J.;
"DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species";
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

EMBL; U87839; AAB94356.1; -;
HSP; Q92956; 1JMA.
GO: GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor.
SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;

Query Match 23.3%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVSGECPCPKSGYRVKEACGEL 70
1 MKSVLYSYILFLSCIIINGRDVTPYAPSGKCKNEYKRNLCCLSCPPGTYSARLDCSK 60
71 TGTVCPCPCPGTYIAHLNGLSKLQCC-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
61 TNTQCTPCGSGTFTSRNNHLPACLSNCRCD--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDGHCAACRAYATSSPGQVKGGTESQDTLCQCPPTGTFSPN-GTLEECQ 180

Db 119 KGSSGCKACVSTKCGIGYGV-SGHTSAGDVICSPCGLTGTYRTVSSADKCE 169

RESULT 15

057284 PRELIMINARY; PRT; 349 AA.
AC 057284;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
CRMB.

Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=203174;

SEQUENCE FROM N.A.
STRAIN-DUBAI-1992 / CP-5, and SOMALIA-1978;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
EMBL; U87840; AAB94357.1; -;
EMBL; U87837; AAB94354.1; -;
HSP; Q92956; 1JMA.
GO: GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 349 AA; 38036 MW; EA412AEE86E090E4 CRC64;

Query Match 23.3%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;
21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVSGECPCPKSGYRVKEACGEL 70
1 MKSVLYSYILFLSCIIINGRDVTPYAPSGKCKNEYKRNLCCLSCPPGTYSARLDCSK 60
71 TGTVCPCPCPGTYIAHLNGLSKLQCC-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
61 TNTQCTPCGSGTFTSRNNHLPACLSNCRCD--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDGHCAACRAYATSSPGQVKGGTESQDTLCQCPPTGTFSPN-GTLEECQ 180

Db 119 KGSSGCKACVSTKCGIGYGV-SGHTSAGDVICSPCGLTGTYRTVSSADKCE 169

Search completed: June 10, 2004, 12:34:03
Job time : 83 secs

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nucleic - nucleic search, using sw model

on: June 10, 2004, 07:19:52 ; Search time 2480 Seconds
(without alignments)
10328.925 Million cell updates/sec

le: US-09-934-289a-19
fect score: 591
quence: 1 agggagcctcctggagactg.....aaaagaagaagccaaagggg 591

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
rched: 3470272 seqs, 21671516995 residues
al number of hits satisfying chosen parameters: 6940544

imum DB seq length: 0
imum DB seq length: 2000000000

it-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_vl:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sta:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rtd:*
36: em_htg_rtd:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	591	100.0	591	6	AR168183	AR168183 Sequence
2	591	100.0	591	6	BD244691	BD244691 Novel mol
3	591	100.0	1596	6	AR168182	AR168182 Sequence
4	591	100.0	1596	6	BD244690	BD244690 Novel mol
5	552.6	93.5	4622	6	AR169917	AR169917 Sequence
6	552.6	93.5	4622	6	AR172621	AR172621 Sequence
7	552.6	93.5	4622	6	AR340583	AR340583 Sequence
8	550.8	93.2	831	6	BD244703	BD244703 Novel mol
9	550.8	93.2	852	9	AF373878	AF373878 Homo sapi
10	550.8	93.2	927	6	BD091696	BD091696 HVM poly
11	550.8	93.2	1049	9	AY358879	AY358879 Homo sapi
12	550.8	93.2	1612	9	BC002794	BC002794 Homo sapi
13	550.8	93.2	1724	6	AR169913	AR169913 Sequence
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26	549.2	92.9	881	9	AF373877	AF373877 Homo sapi
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28	549.2	92.9	1704	6	BD260131	BD260131 Human tum
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35	477.2	80.7	852	9	AF147720	AF147720 Chloroce
36	340.2	57.6	976	6	AR270374	AR270374 Sequence
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43	259.6	43.9	1082	6	AR316349	AR316349 Sequence
44	252.4	42.7	2604	9	AK124010	AK124010 Homo sapi
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ALIGNMENTS

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LOCUS AR168183 591 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 19 from patent US 6287808.
ACCESSION AR168183
VERSION AR168183.1 GI:17904009
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Busfield,S.J.
TITLE Molecules of the herpesvirus-entry-mediator-related protein family
and uses thereof
JOURNAL Patent: US 6287808-A 19 11-SEP-2001;

IRCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1596)
 AUTHORS Busfield, S.J.
 TITLE Molecules of the herpesvirus-entry-mediator-related protein family and uses thereof
 JOURNAL Patent: US 6287808-A 17 11-SEP-2001;
 FEATURES Location/Qualifiers
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 241 GGACCTATATGGCCACCTCAATGGCTTACCAAGTCTGCGAGTCCAAATGTGTGAC 300
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 647 CACGAGCAATTTGGCTTATCATATGTGTGAAAAGAGAAAGCCAGGGG 697

TITLE Novel molecules of the herpesvirus-entry-mediator-related protein family and uses thereof
 JOURNAL Patent: JP 2002529051-A 10 10-SEP-2002;
 COMMENT MILLENNIUM PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002529051-A/10
 PD 10-SEP-2002
 PF 03-SEP-1999 JP 2000568973
 FR 03-SEP-1998 US 09/146950, 29-JUN-1999 US 09/342767 PI
 SAMANTHA J BUSFIELD
 FC C12N15/09, A61K48/00, A61P19/02, A61P29/00, A61P31/10, A61P31/12,
 A61P35/00,
 PC A61P37/02, A61P37/08, C07K14/715, C07K16/28, C12N5/10, C12P21/02,
 C12Q1/02,
 PC C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566// (C12P21/02,
 C12R1:91),
 PC C12N15/00, C12N5/00
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 CC and uses thereof
 FH Key Location/Qualifiers
 PH CDS (107)...(597).
 FT CDS
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 Best Local Similarity 100.0%; Pred. No. 4.8e-114;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 61 TTGAGCTGGTGTGTATCTCACTTTCTGGAGCCCTCTAGCCCGAGCTTGGCG 120
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 121 TCTGCAAGGAGGACAGTACCAGTGGGCTCCGAGTCTGCCCCAGTGCAGTCCAGGT 180
 227 TCTGCAAGGAGGACAGTACCAGTGGGCTCCGAGTCTGCCCCAGTGCAGTCCAGGT 286
 181 TATCGTGTGAAGGAGGCTCGCGGAGCTGAGGGGACAGTGTGTGAACCTTGCCTCCA 240
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 347 GGACCTATATGGCCACCTCAATGGCTTACCAAGTCTGCGAGTCCAAATGTGTGAC 406
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SULT 4
 CDS
 FINITION Novel molecules of the herpesvirus-entry-mediator-related protein family and uses thereof.
 CESSION BD244690
 REGION BD244690.1 GI:33054460
 WORDS JP 2002529051-A/10.
 URCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1596)
 AUTHORS Busfield, S.J.

RESULT 5
LOCUS AR169917 4622 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6291207.
ACCESSION AR169917
VERSION AR169917.1 GI:17907876
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Herpes virus entry receptor protein
JOURNAL Patent: US 6291207-A 6 18-SEP-2001;
FEATURES
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Best Local Similarity 98.4%; Pred. No. 4.6e-106;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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61 TTGAGGCTGTGTATCTACCTTTCTGGAGAGCCCTCTGTAAGCCCGAGCTCTGCCG 120
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DEFINITION Sequence 6 from patent US 630336.
ACCESSION AR172621
VERSION AR172621.1 GI:17912112
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Antibody to Herpes virus entry receptor protein
JOURNAL Patent: US 6573059-A 6 03-JUN-2003;
FEATURES
Location/Qualifiers

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Herpes virus entry receptor protein
JOURNAL Patent: US 630336-A 6 16-OCT-2001;
FEATURES
Location/Qualifiers
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Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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LOCUS AR340583 4622 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6573059.
ACCESSION AR340583
VERSION AR340583.1 GI:33732243
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Antibody to Herpes virus entry receptor protein
JOURNAL Patent: US 6573059-A 6 03-JUN-2003;
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Location/Qualifiers

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BD244703      831 bp      DNA      linear      PAT 17-JUL-2003
Novel molecules of the herpesvirus-entry-mediator-related protein
family and uses thereof.
BD244703
BD244703.1 GI:33054473
Patent: JP 2002529051-A/23.
WORDS      Homo sapiens (human)
JRC      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 831)
Busfield,S.J.
Novel molecules of the herpesvirus-entry-mediator-related protein
family and uses thereof
Patent: JP 2002529051-A 23 10-SEP-2002;
MILLENNIUM PHARMACEUTICALS INC
OS      Homo sapiens (human)
PN      JP 2002529051-A/23
PD      10-SEP-2002
PF      03-SEP-1999 JP 2000568973
PR      03-SEP-1998 US      09/146950,29-JUN-1999 US      09/342767 PI
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SAVANTHA J BUSFIELD
PC      C12N15/09,A61K48/00,A61P19/02,A61P29/00,A61P31/10,A61P31/12,
PC      A61P35/00,
PC      A61P37/02,A61P37/06,C07K14/715,C07K16/28,C12N5/10,C12P21/02,
PC      C12Q1/02,
PC      C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/02,
PC      C12R1/91,
PC      C12N15/00,C12N5/00
CC      Novel molecules of the herpesvirus-entry-mediator-related CC
protein family
CC      and uses thereof Location/Qualifiers
FH      Key
FT      CDS
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LOCUS      Homo sapiens herpesvirus entry mediator (TNFRSF14) mRNA,
DEFINITION      TNFRSF14-V241I allele, complete cds.
ACCESSION      AF373878
VERSION
KEYWORDS      AF373878.1 GI:17901872
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URCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 852)
 AUTHORS Struyf, F., Posavad, C.M., Keyaerts, E., Van Ranst, M., Corey, L. and
 Spear, P.G.
 TITLE Search for Polymorphisms in the Genes for Herpesvirus Entry
 Mediator, Nectin-1, and Nectin-2 in Immune Seronegative Individuals
 J. Infect. Dis. 185 (1), 36-44 (2002)
 JOURNAL 11756979
 PUBLISHED 2 (bases 1 to 852)
 REFERENCE Struyf, F., Posavad, C.M., Keyaerts, E., Van Ranst, M., Corey, L. and
 Spear, P.G.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-2001) Microbiology-Immunology, Northwestern
 University Medical School, 320 E. Superior, Searle 6-447, Chicago,
 IL 60611, USA

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RIGIN

Query Match 93.2%; Score 550.8; DB 9; Length 852;
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 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 b 1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGAGTC 60
 y 61 TTGAGGCTGGTGCTGATCTACCTTTCTGGAGAGCCCTGCTACGCCCGCAGCTCTGCCG 120
 b 61 TTGAGGCTGGTGCTGATCTACCTTTCTGGAGAGCCCTGCTACGCCCGCAGCTCTGCCG 120
 y 121 TCCTGCAAGAGAGAGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCCAGGT 180
 b 121 TCCTGCAAGAGAGAGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCCAGGT 180
 y 181 TATCGTGTGAAGAGAGGCTCGGGGAGCTGACCGGACACAGTGTGTGAACCCCTGCCCTCA 240
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 DEFINITION HVEM polypeptides and uses thereof.
 ACCESSION BD091696
 VERSION BD091696.1 GI:22637307
 KEYWORDS JP 2001526632-A/1.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 927)
 AUTHORS Ashkenazi, A.J. and Marsters, S.A.
 TITLE HVEM polypeptides and uses thereof
 JOURNAL Patent: JP 2001526632-A 1 18-DEC-2001;
 GENENTECH INC
 COMMENT PN JP 2001526632-A/1
 PD 18-DEC-2001
 PP 05-DEC-1997 JP 1998526821
 PR 12-DEC-1996 US 60/032705
 PI AVI J ASHKENAZI, SCOT A MARSTERS
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 CC Topology: Linear;
 FH Key Location/Qualifiers.

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ORIGIN

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 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGAGTC 60
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 AY358879 Homo sapiens clone DNA50148 HVEM (UNQ329) mRNA, complete cds.

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 YKORDS
 TRCE
 ORGANISM
 Homo sapiens
 Homo sapiens (human)

PERENCE
 AUTHORS
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1049)
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B.,
 Dowd,P., Eaton,D., Foster,J.G., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V.,
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 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
 PUBMED
 12975309
 2 (bases 1 to 1049)
 Clark,H.F.
 Direct Submission

TITLE
 Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

JOURNAL
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

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 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12

BC002794

LOCUS

DEFINITION

Homo sapiens tumor necrosis factor receptor superfamily, member 14

(herpesvirus entry mediator), mRNA (cdna clone MGC:3753

IMAGE:3614650), complete cds.

ACCESSION

BC002794

VERSION

BC002794.2

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 1612)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,I., Wang,J., Haileh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,

Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toehiyuki,S.,

Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,

Abramson,K.D., Mullaly,S.J., Bosak,S.A., McMan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE
22388257
12477932

REFERENCE
2 (bases 1 to 1612)

AUTHORS
Straussberg, R.

TITLE
Direct Submission

JOURNAL
Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:12803894.
Contact: MGC help desk
Email: cgapsb-re@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Mastriano, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: TRAL Plate: 12 Row: P Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23200040.

FEATURES
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Best Local Similarity 99.6%; Pred. No. 1.3e-105;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AR169913
Sequence 1 from patent US 6291207.
AR169913
AR169913.1 GI:17907872
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1724)
Spear, P.G. and Montgomery, R.I.
Herpes virus entry receptor protein
Patent: US 6291207-A 1 18-SEP-2001;
Location/Qualifiers
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Best Local Similarity 99.6%; Pred. No. 1.3e-105;
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 ACCESSION BD244687
 VERSION BD244687.1 GI:33054457
 KEYWORDS JP 2002529051-A/7.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 BUSFIELD, S.J.
 Novel molecules of the herpesvirus-entry mediator-related protein
 Patent: JP 2002529051-A 7 10-SEP-2002;
 MILLENNIUM PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002529051-A/7
 PD 10-SEP-2002
 PF 03-SEP-1999 JP 2000568973
 PR 03-SEP-1998 US 09/146950, 29-JUN-1999 US 09/342767 PI
 SAMANTHA J BUSFIELD
 PC C12N15/00, A61K48/00, A61P19/02, A61P29/00, A61P31/10, A61P31/12,
 PC A61P35/00,
 PC A61P37/02, A61P37/08, C07K14/715, C07K16/28, C12N5/10, C12P21/02,
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 FH CDS (294)..(1142).
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 Best Local Similarity 99.6%; Pred. No. 1.3e-105;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 ATGAGGCTCTGGAGACTGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGAGTC 60
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RESULT 15
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 DEFINITION Novel molecules of the herpesvirus-entry mediator-related protein
 ACCESSION BD244687
 VERSION BD244687.1 GI:33054457
 KEYWORDS JP 2002529051-A/7.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 BUSFIELD, S.J.
 Novel molecules of the herpesvirus-entry mediator-related protein
 Patent: JP 2002529051-A 7 10-SEP-2002;
 MILLENNIUM PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002529051-A/7
 PD 10-SEP-2002
 PF 03-SEP-1999 JP 2000568973
 PR 03-SEP-1998 US 09/146950, 29-JUN-1999 US 09/342767 PI
 SAMANTHA J BUSFIELD
 PC C12N15/00, A61K48/00, A61P19/02, A61P29/00, A61P31/10, A61P31/12,
 PC A61P35/00,
 PC A61P37/02, A61P37/08, C07K14/715, C07K16/28, C12N5/10, C12P21/02,
 PC C12Q1/02, G01N33/15, G01N33/50, G01N33/53, G01N33/566, (C12P21/02,
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 PC C12N15/00, C12N5/00
 CC Novel molecules of the herpesvirus-entry mediator-related CC
 protein family
 CC and uses thereof
 CC Key Location/Qualifiers
 FH CDS (294)..(1142).
 FT Location/Qualifiers
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 /organism="Homo sapiens"

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/db_xref="taxon:9606"

Query Match      93.2%; Score 550.8; DB 6; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.3e-105;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGAGCCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGCAGAACCGACGTC 60
2294 ATGGAGCCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGCAGAACCGACGTC 353
61 TTGAGGCTGGTGTATCTATCTCACTTCTGGAGGCCCCCTGCTACGCCCCAGCTCTGCCG 120
354 TTGAGGCTGGTGTATCTATCTCACTTCTGGAGGCCCCCTGCTACGCCCCAGCTCTGCCG 413
121 TCCTCCAGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCCAAAGTCAGTCCAGGT 180
414 TCCTCCAGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCCAAAGTCAGTCCAGGT 473
181 TATCGTGTGAAGGAGGCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCCTGCCCTCCA 240
474 TATCGTGTGAAGGAGGCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCCTGCCCTCCA 533
241 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAAGTCCCAAAATGTGTGAC 300
534 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAAGTCCCAAAATGTGTGAC 593
301 CCAGCCATGGGCTGCGGGGAGCTGCGGGGAGCTGCGGGGAGCTGCGGGGAGCTGCGGGG 360
594 CCAGCCATGGGCTGCGGGGAGCTGCGGGGAGCTGCGGGGAGCTGCGGGGAGCTGCGGGG 653
361 TGCAGCCAGGCGCACTTCTGCACTGCTCCAGGACGGGACCACTCCGCCGCGTCCCGCGCT 420
654 TGCAGCCAGGCGCACTTCTGCACTGCTCCAGGACGGGACCACTCCGCCGCGTCCCGCGCT 713
421 TAGCGCACTTCCAGCCCGGCGCGAGGGGTGCGAGGGAGGCGGACCGAGAGTCCAGGACCC 480
714 TAGCGCACTTCCAGCCCGGCGCGAGGGGTGCGAGGGAGGCGGACCGAGAGTCCAGGACCC 773
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAG 540
774 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAG 833
541 CACCAGACCAATTG 554
834 CACCAGACCAAGTG 847
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Search completed: June 10, 2004, 10:22:35
db time : 2484 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

nucleic - nucleic search, using sw model
on: June 10, 2004, 07:19:52 ; Search time 355 seconds
(without alignments)
7072.352 Million cell updates/sec

file: US-09-934-289a-19
effect score: 591
quence: 1 atggagctctcggagactg.....aaagaagaagcaagggg 591

oring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
arched: 3373863 segs, 2124099041 residues
tal number of hits satisfying chosen parameters: 6747726

imum DB seq length: 0
imum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : N Geneseq 29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	591	100.0	591	7	ABX90566	Abx90566 Human ORF
2	591	100.0	1596	3	Aaz94197	Aaz94197 Soluble h
3	591	100.0	1596	7	ABX90565	Abx90565 Human CDN
4	550.8	93.2	831	7	ABX90578	Abx90578 Human mem
5	550.8	93.2	927	2	AAV44852	AAV44852 Herpesvir
6	550.8	93.2	927	2	AAV44852	AAV44852 CDNA clon
7	550.8	93.2	1049	3	AAV49727	AAV49727 Human PRO
8	550.8	93.2	1049	3	AAV46931	AAV46931 CDNA enco
9	550.8	93.2	1724	6	ABK84410	ABK84410 Human CDN
10	550.8	93.2	1724	7	ABX90562	Abx90562 Human mem
11	550.8	93.2	1724	7	ACC72778	Acc72778 Human can
12	550.8	93.2	1724	7	ABZ99577	Abz99577 Human cob
13	550.8	93.2	1724	8	ADA43034	Ada43034 Human her
14	550.8	93.2	1834	3	Aaz94198	Aaz94198 Membrane-
15	550.8	93.2	1834	7	ABX90577	Abx90577 Human mem
16	550	93.1	579	7	ABX90557	Abx90557 Human ORF
17	550	93.1	1815	4	AAS03021	Aas03021 Human dia
18	550	93.1	1929	3	Aaz94195	Aaz94195 Soluble h
19	550	93.1	1929	7	ABX90556	Abx90556 Human CDN
20	549.2	92.9	881	2	AAT40048	Aat40048 Human tum
21	549.2	92.9	881	3	AAZ28149	Aaz28149 Human TR2
22	549.2	92.9	1704	3	AAA28135	Aaa28135 Human TR2
23	548.4	92.8	558	7	ABX90572	Abx90572 Human ORF

24	548.4	92.8	2313	3	AAZ94197	Aaz94197 Soluble h
25	548.4	92.8	2313	7	ABX90571	Abx90571 Human CDN
26	547.6	92.7	1704	2	AAV34509	Aav34509 Human TNF
27	547.6	92.7	1704	2	AAV83763	Aav83763 Human tum
28	544.4	92.1	1724	2	AAT51737	Aat51737 Human her
29	544.4	92.1	1724	2	AAZ25512	Aaz25512 Herpes vi
30	340.2	57.6	976	7	ACA56339	Aca56339 Human sig
31	309.6	52.4	477	3	AAC04465	Aac04465 Human sec
32	304.6	51.5	723	2	AAT40049	Aat40049 Human tum
33	304.6	51.5	2692	2	AAV34510	Aav34510 Human TNF
34	304.6	51.5	2692	2	AAZ28147	Aaz28147 Human TR2
35	239.4	40.5	2637	2	AAV34511	Aav34511 Human TNF
36	239.4	40.5	2637	2	AAZ28148	Aaz28148 Human TR2
37	233.8	39.6	447	8	ACH16324	Ach16324 Human adu
38	233.4	39.5	405	2	AAT40050	Aat40050 Human tum
39	162.2	27.4	9159	4	AAK83488	Aak83488 Human imm
40	126	21.3	126	7	ABX90575	Abx90575 Human sol
41	126	21.3	126	7	ABX90576	Abx90576 Human sol
42	126	21.3	126	7	ABX90561	Abx90561 Human sol
43	126	21.3	126	7	ABX90560	Abx90560 Human sol
44	126	21.3	126	7	ABX90569	Abx90569 Human sol
45	126	21.3	126	7	ABX90582	Abx90582 Human mem

ALIGNMENTS

RESULT 1
ABX90566
ID ABX90566 standard; cDNA; 591 BP.
XX
AC ABX90566;
XX
DT 06-MAY-2003 (first entry)
XX
DE Human ORF for soluble Herpesvirus Entry Mediator-2 (SHVEM-2).
XX
KW Human; ss: gene: TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.
XX
OS Homo sapiens.
XX
PN US2002132297-A1.
XX
PD 19-SEP-2002.
XX
PF 21-AUG-2001; 2001US-00934289.
XX
PR 03-SEP-1998; 98US-00146950.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ;
XX
DR WPI; 2003-255105/25.
XX
DR P-PSDB; ABU60682.
XX
PT New TANGO-69 receptor polynucleotides and polypeptides, useful for
PT treating arthritis, graft rejection, AIDS, bacterial infection,
PT psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,
PT asthma, psoriasis, lupus.
XX
PS Claim 2; Fig 3; 79pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule, designated as

Query Match	100.0%;	Score 591;	DB 3;	Length 1596;
Best Local Similarity	100.0%;	Pred. No. 7.6e-140;		
Matches 591;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
1	ATGGAGCCTCCCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCCACGTC	60		
107	ATGGAGCCTCCCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCCACGTC	166		
61	TTGAGGCTGGTCTCTATCTACCTTTCTGGGAGCCCTCTGTACGCCCCAGCTCTGGCG	120		
167	TTGAGGCTGGTCTGTATCTACCTTTCTGGAGCCCTCTGTACGCCCCAGCTCTGGCG	226		
121	TCTGTCAAGAGGAGCAGATACCCAGTGGGCTTCCAGTGTCTGCCCCCAAGTGCAGTCCAGGT	180		
227	TCTGTCAAGAGGAGCAGATACCCAGTGGGCTTCCAGTGTCTGCCCCCAAGTGCAGTCCAGGT	286		
181	TATCTGTGTCAAGAGGAGCCTTGGGGGAGCTGACGGGCACAGTGTGTGAACCTCTGCCCTCCA	240		
287	TATCTGTGTGAAGAGGAGCCTTGGGGGAGCTGACGGGCACAGTGTGTGAACCTCTGCCCTCCA	346		
241	GGACCTCAATTTGCCCACTTCAATGGCCCTAAGCAAGTGTCTGCAGTGTGCCAATGTGTGAC	300		
347	GGACCTCAATTTGCCCACTTCAATGGCCCTAAGCAAGTGTCTGCAGTGTGCCAATGTGTGAC	406		
301	CCAGCCATGGGCTCGCGCCGAGCCGGAATCTGCTCCAGGACAGAGAAACGCGTGTGTGGC	360		
407	CCAGCCATGGGCTCGCGCCGAGCCGGAATCTGCTCCAGGACAGAGAAACGCGTGTGTGGC	466		
361	TGAGGCCCAAGGCCATTTCTGCATCTCTCAGAGACGGGACCACTTGGCCCGCTGCCCGCT	420		
467	TGAGGCCCAAGGCCATTTCTGCATCTCTCAGAGACGGGACCACTTGGCCCGCTGCCCGCT	526		
421	TAGGCCACCTTCCAGCCCGGGCCAGAGGGTGTGAGAAGGGAGGCCACCGAGAGTCAAGGACCC	480		
527	TAGGCCACCTTCCAGCCCGGGCCAGAGGGTGTGAGAAGGGAGGCCACCGAGAGTCAAGGACCC	586		
481	CTGTGTGAGAACTGCGCCCGGGGACCTTCTCTCCCAATGGGACCTCTGGAGGAATGTCTGAG	540		
587	CTGTGTGAGAACTGCGCCCGGGGACCTTCTCTCCCAATGGGACCTCTGGAGGAATGTCTGAG	646		
541	CACGAGACCAATTTGGCCTAATCATATGTGTGAAAAGAGAAAGCCAAAGGGG	591		
647	CACGAGACCAATTTGGCCTAATCATATGTGTGAAAAGAGAAAGCCAAAGGGG	697		

SULT 3
X90565

ABX90565 standard; cDNA; 1596 BP.

ABX90565;

06-MAY-2003 (first entry)

Human cDNA encoding soluble Herpesvirus Entry Mediator-2 (sHVM-2).

Human; ss: gene; TANGO-69 human; herpesvirus entry mediator; HVEM; SHVEM1; SHVEM2; HVEM2; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicæmia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder; asthma; psoriasis; apoptotic disorder; rheumatoid arthritis; systemic lupus erythematosus; insulin-dependent diabetes mellitus; cytotoxic disorder; septic shock; cachexia; proliferative disorder; B-cell cancer.

Homo sapiens.

US2002132297-A1.

19-SEP-2002.

21-AUG-2001; 2001US-00934289.

XX	03-SEP-1998;	98US-00146950.	
XX	(MILL-) MILLENNIUM PHARM INC.		
XX	Busfield SJ;		
XX	WPI; 2003-255106/25.		
XX	P-PSDB; ABU60682.		
XX	New TANGO-69 receptor polynucleotides and polypeptides, useful for		
XX	treating arthritis, graft rejection, AIDS, bacterial infection,		
XX	psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,		
XX	asthma, psoriasis, lupus.		
XX	Claim 2; Fig 3; 79pp; English.		
XX	The invention relates to an isolated nucleic acid molecule, designated as		
XX	TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion		
XX	of the proteins sHVE1, sHVE2, sHVE3 and mHVE2 (where HVE1 is		
XX	Herpesvirus Entry Mediator and "g" refers to a soluble form and "m" to a		
XX	membrane bound form). Also included are a host cell containing TANGO-69		
XX	receptor nucleic acid, a non-human mammalian host cell containing TANGO-		
XX	69 receptor nucleic acid, an isolated polypeptide that is encoded by		
XX	TANGO-69 receptor nucleic acid, an antibody that selectively binds to the		
XX	TANGO-69 receptor polypeptide, and identifying a compound that binds to		
XX	and/or modulates the activity of the TANGO-69 receptor polypeptide. The		
XX	polynucleotides, polypeptides compounds and methods are useful for		
XX	treating immune disorders such as autoimmune disorders (e.g. arthritis,		
XX	graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g.		
XX	bacterial infection, psoriasis, septicemia, cerebral malaria,		
XX	inflammatory bowel disease, rheumatoid arthritis, osteoarthritis),		
XX	allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic		
XX	disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus,		
XX	insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,		
XX	cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69		
XX	receptor is a member of the TNF (tumour necrosis factor) superfamily of		
XX	proteins. The present sequence encodes a TANGO-69 receptor protein		
XX	Sequence 1596 BP; 341 A; 485 C; 483 G; 287 T; 0 U; 0 Other;		
XX	Query Match 100.0%; Score 591; DB 7; Length 1596;		
XX	Best Local Similarity 100.0%; Pred. No. 7.6e-140;		
XX	Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGGAGCTCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCAGAACCGACGTC 60	
QY	107	ATGGAGCTCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCAGAACCGACGTC 166	
QY	61	TTGAGCTGTGTGTATCTCACTCTTCTGGAGCCCTCTGTACGCCCAAGCTCTGGCG 120	
QY	167	TTGAGCTGTGTGTATCTCACTCTTCTGGAGCCCTCTGTACGCCCAAGCTCTGGCG 226	
QY	121	TCTTCAGAGGACGAGTACCAAGTGGCTCCAGTGTGTGCCCAAGTGCAGTCCAGGT 180	
QY	227	TCTTCAGAGGACGAGTACCAAGTGGCTCCAGTGTGTGCCCAAGTGCAGTCCAGGT 286	
QY	181	TATCTGTGTGAAGGAGGCTCTGGGGAGCTGACGGGCACAGTGTGTGAACCTTGCCTCCA 240	
QY	287	TATCTGTGTGAAGGAGGCTCTGGGGAGCTGACGGGCACAGTGTGTGAACCTTGCCTCCA 346	
QY	241	GGCACCCTACATTGGCCACTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 300	
QY	347	GGCACCCTACATTGGCCACTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 406	
QY	301	CCAGCCATTGGGCTCTGGCGCGAGCCGGAACTGTCTCAGGACAGAGAACCGCTGTGTGGC 360	
QY	407	CCAGCCATTGGGCTCTGGCGCGAGCCGGAACTGTCTCAGGACAGAGAACCGCTGTGTGGC 466	
QY	361	TGCAGCCAGGCGCACTTGTGATCTGCAGACGGGACCACTTGGCGCGGTGCGCGGCT 420	
QY	467	TGCAGCCAGGCGCACTTGTGATCTGCAGACGGGACCACTTGGCGCGGTGCGCGGCT 526	

Y 421 TAGCCACCTCCAGCCCGGCGGAGAGGTGCAGAGGAGGACCGAGAGTCAGGACACC 480
b 527 TAGCCACCTCCAGCCCGGCGGAGAGGTGCAGAGGAGGACCGAGAGTCAGGACACC 586
Y 481 CTGTGTGAGAACTGCCCGCCCGGCGGACCTTCTCTCCCAATGGAGACCTCGGAGGAATGTGAG 540
b 587 CTGTGTGAGAACTGCCCGCCCGGCGGACCTTCTCTCCCAATGGAGACCTCGGAGGAATGTGAG 646
Y 541 CACGAGACCAATGGCCCTAATCATATGTGTGAAAGAGAGAAAGCCAGGGG 591
b 647 CACGAGACCAATGGCCCTAATCATATGTGTGAAAGAGAGAAAGCCAGGGG 697

RESULT 4

BX90578

D ABX90578 standard; cDNA; 831 BP.

X C ABX90578;

X X 06-MAY-2003 (first entry)

X T Human membrane-bound Herpesvirus Entry Mediator-2 (mHVEM-2) ORF.

X E Human; ss; gene; TANGO-69 receptor; herpesvirus entry mediator; HVEM;

X W SHVEM1; SHVEM2; mHVEM2; tumour necrosis factor receptor; TNFR;

X W immune disorder; autoimmune disorder; arthritis; graft rejection;

X W T-cell disorder; AIDS; inflammatory disorder; bacterial infection;

X W psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;

X W rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;

X W asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;

X W systemic lupus erythematosus; insulin-dependent diabetes mellitus;

X W cytotoxic disorder; septic shock; cachexia; proliferative disorder;

X W B-cell cancer.

X W Homo sapiens.

X S US2002132297-A1.

X N 19-SEP-2002.

X D 21-AUG-2001; 2001US-00934289.

X F 03-SEP-1998; 98US-00146950.

X R (MILL-) MILLENNIUM PHARM INC.

X A Busfield SJ;

X X WPI: 2003-255106/25.

X R P-PSDB; ABU60694.

X X Claim 2; Fig 7; 79pp; English.

X S The invention relates to an isolated nucleic acid molecule, designated as

X C TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion

X C of the proteins SHVEM1, SHVEM2, mHVEM2 and mHVEM2 (where HVEM is

X C Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

X C membrane bound form). Also included are a host cell containing TANGO-69

X C receptor nucleic acid, a non-human mammalian host cell containing TANGO-

X C 69 receptor nucleic acid, an isolated polypeptide that is encoded by

X C TANGO-69 receptor nucleic acid, an antibody that selectively binds to the

X C TANGO-69 receptor polypeptide, and identifying a compound that binds to

X C and/or modulates the activity of the TANGO-69 receptor polypeptide. The

X C polynucleotides, polypeptides compounds and methods are useful for

X C treating immune disorders such as autoimmune disorders (e.g. arthritis,

X C graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g.

X C bacterial infection, psoriasis, septicemia, cerebral malaria, inflammation,

X C inflammatory bowel disease, rheumatoid arthritis, osteoarthritis),

CC allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic
CC disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus,
CC insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,
CC cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69
CC receptor is a member of the TNF (tumour necrosis factor) superfamily of
CC proteins. The present sequence encodes a TANGO-69 receptor protein
XX
SQ Sequence 831 BP; 149 A; 274 C; 246 G; 162 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 7; Length 831;

Best Local Similarity 99.6%; Pred. No. 1e-129;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCGAGAACCGAGCTC 60

Db 1 ATGGAGCCTCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCGAGAACCGAGCTC 60

QY 61 TTGAGGCTGGTGTGTATCTACCTTTCTGGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCG 120

Db 61 TTGAGGCTGGTGTGTATCTACCTTTCTGGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCG 120

QY 121 TCTTGAAGGAGGAGAGTACCCAGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Db 121 TCTTGAAGGAGGAGAGTACCCAGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

QY 181 TATCGTGTGAAGGAGGCT 240

Db 181 TATCGTGTGAAGGAGGCT 240

QY 241 GCACACTCATTTGCCACCT 300

Db 241 GCACACTCATTTGCCACCT 300

QY 301 CCAGCCATGGGCT 360

Db 301 CCAGCCATGGGCT 360

QY 361 TGCAGCCAGGAGGCT 420

Db 361 TGCAGCCAGGAGGCT 420

QY 421 TAGCCACCTCTCCAGCCCGGCGGAGAGGTGCAGAGGAGGACCGAGAGTCAGGACACC 480

Db 421 TAGCCACCTCTCCAGCCCGGCGGAGAGGTGCAGAGGAGGACCGAGAGTCAGGACACC 480

QY 481 CTGTGTGAGAACTGCCCGCCCGGCGGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540

Db 481 CTGTGTGAGAACTGCCCGCCCGGCGGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540

QY 541 CACGAGACCAATTTG 554

Db 541 CACGAGACCAATTTG 554

RESULT 5

AAV44852

ID AAV44852 standard; DNA; 927 BP.

XX AC AAV44852;

XX DT 17-OCT-2003 (revised)

XX DT 21-OCT-1998 (first entry)

XX DE Herpesvirus entry mediator gene.

XX KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;

XX KW gene expression regulator; cellular stress; inflammatory response;

XX KW lymphocyte activity regulator; autoimmune response; ds.

XX OS unidentified herpesvirus.

XX PH Key Location/Qualifiers

XX FT CDS 76..927

/*tag= a
/product= "HVEM"

WO9825967-A1.

18-JUN-1998.

05-DEC-1997; 97WO-US022278.

12-DEC-1996; 96US-0032705P.

(GETH) GENENTECH INC.

Askenazi AJ, Marsters SA;

WPI; 1998-348457/30.

P-PSDB; AAW69238.

Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for HVEM and to produce antibodies and transgenic animals, e.g. for drug screening.

Example 1; Fig 1; 46pp; English.

This sequence encodes the herpesvirus entry mediator (HVEM) protein of the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain transcription factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of therapeutically useful reagents. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 2; Length 927;
Best Local Similarity 99.6%; Pred. No. 1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTGGAGATGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGTC 60
76 ATGGAGCTCTGGAGATGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGTC 135
61 TTGAGGCTGTGTCTATCTATCTCTGAGGAGCCCTCTGAGCCCGAGCTCTGCG 120
136 TTGAGGCTGTGTCTATCTATCTCTGAGGAGCCCTCTGAGCCCGAGCTCTGCG 195
121 TCTTCAAGGAGGACGATACCCAGTGCGCTCCAGTGCTGCCCGAACGATCCAGGT 180
196 TCTTCAAGGAGGACGATACCCAGTGCGCTCCAGTGCTGCCCGAACGATCCAGGT 255
181 TATCTGTGTGAGGAGGCTCGGGGAGCTGACGGGACAGTGCTGAACTCCCTCCA 240
256 TATCTGTGTGAGGAGGCTCGGGGAGCTGACGGGACAGTGCTGAACTCCCTCCA 315
241 GGCACCTACATTGCCACCTCAATGGCCCTAAGCAAGTGCTTGCAGTGCCAAATGTGTAC 300
316 GGCACCTACATTGCCACCTCAATGGCCCTAAGCAAGTGCTTGCAGTGCCAAATGTGTAC 375

QY 301 CCAGCCATGGGCTGCGCGAGCCGGAATCTGCTCCAGGACAGAGAACCCGCTGTGTGC 360
DB 376 CCAGCCATGGGCTGCGCGAGCCGGAATCTGCTCCAGGACAGAGAACCCGCTGTGTGC 435
QY 361 TGCAGCCAGGCACTTCTGCACTGTCAGGACGGGACCACTGCGCCCGCTGCCCGCT 420
DB 436 TGCAGCCAGGCACTTCTGCACTGTCAGGACGGGACCACTGCGCCCGCTGCCCGCT 495
QY 421 TAGCCACCTCCAGCCCGGGCCAGAGGTCGACAGAGGAGGACCCAGAGAGTCAGGACAC 480
DB 496 TAGCCACCTCCAGCCCGGGCCAGAGGTCGACAGAGGAGGACCCAGAGAGTCAGGACAC 555
QY 481 CTGTGTCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
DB 556 CTGTGTCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 615
QY 541 CACCAGACCAATTG 554
DB 616 CACCAGACCAATTG 629

RESULT 6

AAX87265
ID AAX87265 standard; CDNA; 927 BP.

AC AAX87265;

DT 27-SEP-1999 (first entry)

DE CDNA clone encoding human PRO509, amplified in tumour cells.

KW PRO509; UNQ329; tumour necrosis factor receptor; cancer; diagnosis;
KW therapy; human; HVEM; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 76..927
FT /*tag= a

XX WO9935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999; 99WO-US000106.

XX 05-JAN-1998; 98US-0070440P.

XX 29-APR-1998; 98US-0083500P.

XX 22-MAY-1998; 98US-0086414P.

XX 10-JUN-1998; 98US-0088742P.

XX 10-NOV-1998; 98US-0107783P.

XX 20-NOV-1998; 98US-0109304P.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;

XX Wood WI;

XX WPI; 1999-430385/36.

XX P-PSDB; AAY06488.

XX Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment.

XX Example 1; Fig 23; 162pp; English.

XX This is the nucleotide sequence of cDNA clone DNA50148 (HVEM) coding for human PRO509 (UNQ329) (see AAY06488), a member of the tumour necrosis factor receptor family. Amplification of DNA50148 occurs in various CC tumours, suggesting an association with tumour formation or growth. CC Antagonists (e.g. antibodies) directed to PRO509 may have use in cancer CC therapy. The invention identifies 14 genes (see AAX87254-67) that are

IC amplified in the genome of tumour cells. Such amplification is expected
XC to be associated with overexpression of the gene product and to
XC contribute to tumorigenesis. The encoded proteins (see AA06477-90) may
XC be useful targets for the diagnosis and/or treatment (including
XC prevention) of certain cancers, and may act as predictors of the
XC prognosis of tumour treatment
X
Q Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 2; Length 927;
Best Local Similarity 99.6%; Pred. No. 1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 1 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
b 76 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 135
Y 61 TTGAGGCTGGTGTATCTACCTTTCTGGAGGCCCCCTGTACGCCCCGAGCTTGCGG 120
b 136 TTGAGGCTGGTGTATCTACCTTTCTGGAGGCCCCCTGTACGCCCCGAGCTTGCGG 195
Y 121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTCAGTCCAGGT 180
b 196 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTCAGTCCAGGT 255
Y 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGAGCGGCACAGTGTGTGAACCTTGCCCTCCA 240
b 256 TATCGTGTGAAGAGGCTCTGGGGAGCTGAGCGGCACAGTGTGTGAACCTTGCCCTCCA 315
Y 241 GGCACCTACATTGGCCACCTCAATGGCCTTAAGCAAGTGTCTCAGTGCCTCAATGTGTGAC 300
b 316 GGCACCTACATTGGCCACCTCAATGGCCTTAAGCAAGTGTCTCAGTGCCTCAATGTGTGAC 375
Y 301 CCAGCCATGGGCTGCGCGGAGCCGGAAGTCTCCAGGACAGAGAACGCCGTGTGTGGC 360
b 376 CCAGCCATGGGCTGCGCGGAGCCGGAAGTCTCCAGGACAGAGAACGCCGTGTGTGGC 435
Y 361 TGCAGCCAGGACCACTTCTCATCTGTCAGGAGCGGACCACTGCGCGCGCTGCGCGCT 420
b 436 TGCAGCCAGGACCACTTCTCATCTGTCAGGAGCGGACCACTGCGCGCGCTGCGCGCT 495
Y 421 TAGCCACCTCCAGCCGCGGAGGGGTGCAGAGGGAGGACCGAGAGTCAGACACACC 480
b 496 TAGCCACCTCCAGCCGCGGAGGGGTGCAGAGGGAGGACCGAGAGTCAGACACACC 555
Y 481 CTGTGTGAGAACTGCCCGCGGAGCTTCTCTCCCAATGGGACCTGGAGGAATGTGAG 540
b 556 CTGTGTGAGAACTGCCCGCGGAGCTTCTCTCCCAATGGGACCTGGAGGAATGTGAG 615
Y 541 CACCAGACCAATTG 554
b 616 CACCAGACCAAGTG 629

RESULT 7

AAA49727
D AAA49727 standard; cdna; 1049 BP.
X
C AAA49727;
X
T 25-SEP-2000 (first entry)
X
E Human PRO509 cdna clone DNA50148-1068.
X
W PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer;
W ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
W prostate cancer; lung cancer; bladder cancer;
W central nervous system cancer; melanoma; leukaemia; neoplasm; ss.
X
S Homo sapiens.
X
H Key Location/Qualifiers
T CDS 82..933

FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
XX
PN WO200037638-A2.
XX
XX 29-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US028565.
XX
XX 22-DEC-1998; 98US-0113296P.
PR 08-MAR-1999; 99WO-US005028.
PR 21-APR-1999; 98US-0130232P.
PR 28-APR-1999; 98US-013445P.
PR 14-MAY-1999; 99US-0134287P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
XX
XX (GETH) GENENTECH INC.
PA
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
XX Napier MA, Pitti RM, Wood WI;
PI
XX WPI; 2000-442668/38.
XX
XX P-PSDB; AAY95348.
DR
XX
XX Novel composition to inhibit neoplastic cell growth or for treating tumor
PT in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,
PT PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866.
XX
XX Claim 20; Fig 23; 172pp; English.
XX
XX The present sequence is that of cdna clone DNA50148-1068 encoding human
CC PRO509 (see AA195348), a novel antitumour protein that shows homology to
CC the tumour necrosis factor receptor family. The cdna was isolated from a
CC human retina cdna library by hybridisation. A claimed method for
CC inhibiting the growth of a tumour cell comprises exposing the tumor cell
CC to PRO179, PRO207, PRO320, PRO219, PRO224, PRO328, PRO301,
CC PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their
CC agonists or chimeric polypeptides incorporating them. The tumour is
CC especially a cancer selected from breast, ovarian, renal, colorectal,
CC uterine, prostate, lung, bladder and central nervous system cancer,
CC melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in
CC the recombinant production of the antitumour polypeptides
XX
SQ Sequence 1049 BP; 208 A; 330 C; 332 G; 179 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 3; Length 1049;
Best Local Similarity 99.6%; Pred. No. 1.1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
DB 82 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 141
QY 61 TTGAGGCTGGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCCGAGCTTGCGG 120
DB 142 TTGAGGCTGGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCCGAGCTTGCGG 201
QY 121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCAGTCCAGGT 180
DB 202 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCAGTCCAGGT 261
QY 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCCTCCA 240
DB 262 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCCTCCA 321
QY 241 GGCACCTACATTGCCCGACCTCAATGCGCTTAAGCAAGTGTCTCAGTGCCTCAATGTGTGAC 300

322 GGCACCTCATTTGCCCACTCAATGCCCTTAAGCAAGTGTCTGCAGTGCACAAATGTGTGAC 381

301 CCAGGCATGGGCGCTGCGCGAGAGCGGGAACCTGCTCCAGGACAGAGAAACGCCGTGTGTGAC 360

382 CCAGGCATGGGCGCTGCGCGAGAGCGGGAACCTGCTCCAGGACAGAGAAACGCCGTGTGTGAC 441

361 TGCAGCCCAAGGCCATTCTTGCAATCGTCCAGGACGGGGACCACTGCGCCGCGTGC CGCGCT 420

442 TGCAGCCCAAGGCCATTCTTGCAATCGTCCAGGACGGGGACCACTGCGCCGCGTGC CGCGCT 501

421 TACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAAGGGAGGCAACCGAGAGTCAGGACACC 480

502 TACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAAGGGAGGCAACCGAGAGTCAGGACACC 561

481 CTGTGTGAAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCTAG 540

562 CTGTGTGAAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCTAG 621

541 CACCGACCAATTG 554

622 CACCGACCAAGTG 635

SULT 8
A46931

AAA46931 standard; cDNA: 1049 bp.

AAA46931;

03-OCT-2000 (first entry)

cdNA encoding novel polypeptide PRO509.

PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715;
PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis;
cancer; neoplastic cell growth; cell proliferation; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	82..933
	/*tag= a

WO200037640-A2.

29-JUN-2000.

16-DEC-1999; 99WO-US030095.

22-DEC-1998; 98US-0113296P.

08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.

01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021090

30-NOV-1999; 99WO-US028313.
30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028565

(CENTH) GENENTECH INC

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WPI; 2000-452188/39.

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new anti-polypeptide
neoplastic cell g

Claim 50: Fig 23: 220pp: English.

The present sequence encodes a novel human polypeptide. The specification

describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO503, PRO553 and PRO682. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumorigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals

Query Match 93.2%; Score 550.8; DB 3; Length 1049;
Best Local Similarity 99.6%; Pred. No. 1.1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy	Qy	Db	Qy	Db
1	ATGAGGCTCTCTGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGAGCTC	60	61	TTGAGGCTGGTGCTGTATCTCACCTTTCTGGGAGCCCTCTGCTACGCCCCAGCTCTGGCG
82	ATGAGGCTCTCTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGAGCTC	141	142	ATGAGGCTGGTGCTGTATCTCACCTTTCTGGGAGCCCTCTGCTACGCCCCAGCTCTGGCG

QY	121	TCCTGCAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGGT	180
Db	202	TCCTGCAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGGT	261
QY	181	TATCTGTGTGAAGGAGGCGCTGCGGGAGCTGACGGGCACAGTGTGTGAAACCTTGCCTCCA	240
Db	262	TATCTGTGTGAAGGAGGCGCTGCGGGAGCTGACGGGCACAGTGTGTGAAACCTTGCCTCCA	321
QY	241	GGCACCTACATTGCCCACTTCATATGGCCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC	300
Db	322	GGCACCTACATTGCCCACTTCATATGGCCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC	381
QY	301	CCAGCCATGTGGCCTGCGCGGAGCCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGGC	360
Db	382	CCAGCCATGTGGCCTGCGCGGAGCCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGGC	441
QY	361	TGCAGCCCAAGGCCACTTCTGTGATCGTCCAGGACGGGACCACTGCGCCGCGTGC CGCGT	420
Db	442	TGCAGCCCAAGGCCACTTCTGTGATCGTCCAGGACGGGACCACTGCGCCGCGTGC CGCGT	501
QY	421	TACGGCACTTCAGCCCGGGCCAGAGGGTGCAGAGGGAGGCACCGAGTTCAGGACACC	480
Db	502	TACGGCACTTCAGCCCGGGCCAGAGGGTGCAGAGGGAGGCACCGAGTTCAGGACACC	561
QY	481	CNTGTGTCAAGACTGCCCGCGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAG	540
Db	562	CNTGTGTCAAGACTGCCCGCGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAG	621
QY	541	CACCAGACCAATTG	554
Db	622	CACCAGACCAATTG	635

RESULT 9

RESULT 9
ABK84410

ABK84410
ID ABK84410 standard; cDNA; 1724 BP.

XX ABK84410:

XX
DT 14-AUG-20XX
 11.11.11
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100

KW viral inf

KW
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rheumatoid
rheumatoid

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MY
CROSSING

granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 981; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GCA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in an electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences

Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 6; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTGAGACTGGGGCTCTCTCTGAGATCCACCCCGAGACCGACGTC 60

294 ATGAGGCTCTGAGACTGGGGCTCTCTCTGAGATCCACCCCGAGACCGACGTC 353

61 TTGAGGCTGGGCTGATCTACCTTTCTGGAGCCCTCTGACCCCGAGCTTGGCG 120

354 TTGAGGCTGGGCTGATCTACCTTTCTGGAGCCCTCTGACCCCGAGCTTGGCG 413

QY 121 TCCTCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 180
DB 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 473
QY 181 TATCGTGTAAAGGAGGCTCGGGGAGCTGACGGGCAAGTGTGTGAACCTGCCCTCCA 240
DB 474 TATCGTGTAAAGGAGGCTCGGGGAGCTGACGGGCAAGTGTGTGAACCTGCCCTCCA 533
QY 241 GGCACCTACATTGCCCACTCAATGGGCTTAAGCAAGTGTCTGCAGTGCCTCAAAATGTGTAC 300
DB 534 GGCACCTACATTGCCCACTCAATGGGCTTAAGCAAGTGTCTGCAGTGCCTCAAAATGTGTAC 593
QY 301 CCAGCCATGGGCTCGGGCGAGCCGGAACCTGCTCCAGGACAGAGACGCGGTGTGGC 360
DB 594 CCAGCCATGGGCTCGGGCGAGCCGGAACCTGCTCCAGGACAGAGACGCGGTGTGGC 653
QY 361 TGCAGCCAGGACCTTCTGATGCTCCAGGACGGGACCACTGCGCGCGGTGTGGC 420
DB 654 TGCAGCCAGGACCTTCTGATGCTCCAGGACGGGACCACTGCGCGCGGTGTGGC 713
QY 421 TACGCCACCTCCAGCCCGGGCCAGAGGTGAGAGGAGGACCGGAGAGTCAGGACACC 480
DB 714 TACGCCACCTCCAGCCCGGGCCAGAGGTGAGAGGAGGACCGGAGAGTCAGGACACC 773
QY 481 CTGTGTCAAGTGCCTCGGGCGAGCCGGAACCTTCTCCCAATGGGACCTGGAGGAATGTGAC 540
DB 774 CTGTGTCAAGTGCCTCGGGCGAGCCGGAACCTTCTCCCAATGGGACCTGGAGGAATGTGAC 833
QY 541 CACCAGACCAATTG 554
DB 834 CACCAGACCAAGTG 847

RESULT 10

ABX90562

ID ABX90562 standard; CDNA; 1724 BP.

XX AC ABX90562;

XX DT 06-MAY-2003 (first entry)

XX DE Human membrane-bound Herpesvirus Entry Mediator (mHVM) CDNA.

XX KW Human; ss; gene; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW sHVM1; sHVM2; HVEM3; mHVM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.

XX OS Homo sapiens.

XX PN US2002132297-A1.

XX PD 19-SEP-2002.

XX PF 21-AUG-2001; 2001US-00934289.

XX PR 03-SEP-1998; 98US-00146950.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ;

XX DR WPI; 2003-255106/25.

XX DR P-PSDE; ABU60681.

XX PT New TANGO-69 receptor polynucleotides and polypeptides, useful for

034 CACCAZACCAZIG 04 /

1 ATGGAGCCTCCTGGAGACTGGGGGCTCCTCCCTGGAGATCCACCCAGAACCGACGTC 60

1 ATGGAGCCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCCAGAACCGACGTC 60

1 ATGGAGCCTCCTGGAGACTGGGGGCTCCTCCCTGGAGATCCACCCAGAACCGACGTC 60

541 CACCAGACCAATTG 554
|||||
834 CACCAGACCAAGTG 847

ULT 13
43034
ADA43034 standard; DNA; 1724 BP.

ADA43034;

20-NOV-2003 (first entry)

Human herpesvirus entry mediator (HVEM) gene for myeloma detection.

ds; gene: multiple myeloma; MGUS;
monoclonal gammopathy of undetermined significance;
plasma cell leukemia; WEEL; HVEM; human herpesvirus entry mediator;
histone H2A; LD78alpha; GIPR;
glucose-dependent insulinotropic polypeptide receptor; CTGF;
connective tissue growth factor; cytochrome b alpha-subunit;
major histocompatibility complex; MHC homologue;
thyroid hormone binding protein; THBP; cysteine-rich heart protein; CRHP;
liposome protein L28; growth factor receptor; immunoglobulin;
liposome receptor; liposome protein L18; NM23-H1; heat-shock protein;
laminin receptor; macrophage motility inhibitory factor;
K1AA1042 protein; APR peptide; RING6; human H-factor.

Human herpesvirus.

Key Location/Qualifiers
CDS 294..1145
/*tag= a

/product= "Human herpesvirus entry mediator protein"

WO2003038088-A1.

08-MAY-2003.

30-OCT-2002; 2002WO-JP011257.

02-NOV-2001; 2001JP-00337752.

(FUJI) FUJISAWA PHARM CO LTD.

Mano H;

WPI; 2003-430523/40.
P-PSDB; ADA43035.

Comparison of gene expression profile in tissue sample with known
profiles of normal and pathological tissue for determination of presence
and progression stage of multiple myeloma.

Disclosure; Page 79-82; 128pp; Japanese.

The invention relates to a method for the investigation of multiple
myeloma in which the expression level of genes associated with multiple
myeloma in a sample is compared with that in normal tissue or in MGUS
(monoclonal gammopathy of undetermined significance), MM (multiple
myeloma) or PCL (plasma cell leukaemia) stage multiple myeloma tissue.
The genes compared in the method include one or more of WEEL, HVEM,
histone H2A, LD78alpha, GIPR, CTGF, cytochrome b alpha-subunit, MHC
homologues, THBP, CRHP, liposome protein L28, growth factor receptor,
immunoglobulin Ig lambda-chain, laminin receptor, liposome protein L18,
NM23-H1, 28kDa heat-shock protein, immunoglobulin transcript 3 protein
variant 1, Gsgr binding protein alpha-subunit, M9 macrophage motility
inhibitory factor, K1AA1042 protein, APR peptide, RING6, human H-factor
homologues and K1AA0832 protein genes. The method is useful for the
determination of the existence or stage of progression of multiple
myeloma and the risk of its development, and screening substances for
their ability to treat or prevent multiple myeloma. This sequence

CC represents the human herpesvirus entry mediator (HVEM) gene used in the
CC method of the invention.

XX Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 8; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGAGGCTCTCGAGACTGGGGCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 60
Db 294 ATGGAGGCTCTCGAGACTGGGGCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 353

QY 61 TTGAGGCTGGTGTATCTCACCTTTCTGGAGCCCTCTACGCCCCAGTCTGCGG 120
Db 354 TTGAGGCTGGTGTATCTCACCTTTCTGGAGCCCTCTACGCCCCAGTCTGCGG 413

QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCAAGTCCAGGT 180
Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCAAGTCCAGGT 473

QY 181 TATCGTGTGAAGGAGGCTCGGGGAGCTCACGGGACAGTGTGTGAACCTTCCCTCCA 240
Db 474 TATCGTGTGAAGGAGGCTCGGGGAGCTCACGGGACAGTGTGTGAACCTTCCCTCCA 533

QY 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
Db 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 593

QY 301 CCAGCCATGGGCTCGGGGAGCGGGAATGTCTCCAGGACAGAGAACGCGTGTGTGGC 360
Db 594 CCAGCCATGGGCTCGGGGAGCGGGAATGTCTCCAGGACAGAGAACGCGTGTGTGGC 653

QY 361 TGCAGCCCGAGGCGCACTTCTGCAATGTCAGGACGGGACCACTCGCGCGGTGCGCGCT 420
Db 654 TGCAGCCCGAGGCGCACTTCTGCAATGTCAGGACGGGACCACTCGCGCGGTGCGCGCT 713

QY 421 TACGCCACTTCAGCCCGGCGCAGAGGTGAGAGGAGGACCGAGAGTCAAGACACC 480
Db 714 TACGCCACTTCAGCCCGGCGCAGAGGTGAGAGGAGGACCGAGAGTCAAGACACC 773

QY 481 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 540
Db 774 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 833

QY 541 CACCAGACCAATTG 554

Db 834 CACCAGACCAAGTG 847

RESULT 14

AAZ94198

ID AAZ94198 standard; cDNA; 1834 BP.

XX AC AAZ94198;

XX DT 19-JUN-2000 (first entry)

XX DE Membrane-bound herpesvirus entry mediator-2 (mHVEM2) cDNA.

XX KW mHVEM-2; Membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor;
tumour necrosis factor receptor; human; herpes simplex virus; infection;
cancer; inflammation; autoimmune disorder; therapy; diagnosis; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers
FT CDS 103..936
FT /*tag= a

FT FT 2" /*tag= "this coding region is separately claimed in Claim
FT sig_peptide 103..206
FT /*tag= b

mat_peptide 207..933
/*tag= C

WO200014230-A1.

16-MAR-2000.

03-SEP-1999; 99WO-US020180.

03-SEP-1998; 98US-00146950.

29-JUN-1999; 99US-00342767.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Busfield SJ;

WPI; 2000-256981/22.

P-PSDB; AAY79207.

New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays.

Claim 2; Fig 7; 149pp; English.

This full-length DNA sequence, the coding region of which is also claimed, corresponds to cDNA encoding human membrane-bound herpesvirus entry mediator-2 (mhVEM2, see AAY79207), a novel form of membrane-bound herpesvirus entry mediator (mhVEM). mhVEM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TNFR) superfamily. The mhVEM2 cDNA, deposited as ATCC 207171, was identified in a human mixed lymphocyte reaction library. HVEM mediates the entry of herpes simplex virus (HSC) into cells. The invention is based on the discovery of 3 cDNA molecules (see AAZ94195-97) which encode soluble forms (see AAY79204-06) of mhVEM, and on the present cDNA encoding mhVEM2. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders

Sequence 1834 BP; 398 A; 556 C; 539 G; 341 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 3; Length 1834;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2Y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGAGTC 60
2b 103 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGAGTC 162
2Y 61 TTGAGCTGTGTGTATCTACCTTCTGGAGCCCTCTGGAGCCCTCTGGAGCCCTCTGGAG 120
2b 163 TTGAGCTGTGTGTATCTACCTTCTGGAGCCCTCTGGAGCCCTCTGGAGCCCTCTGGAG 222
2Y 121 TCTCTCAAGGAGGACGAGTACCCAGTGGGCTCTGGAGTGTCTGGAGTGTCTGGAGTGTCT 180
2b 223 TCTCTCAAGGAGGACGAGTACCCAGTGGGCTCTGGAGTGTCTGGAGTGTCTGGAGTGTCT 282
2Y 181 TATCTGTGTGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCTCCCA 240
2b 283 TATCTGTGTGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCTCCCA 342
2Y 241 GGCACCTATTTGCCCACTTCAATGGCGCTTAAGCAAGTGTGTCTGAGTGTCCAAATGTGTGAC 300

Db 343 GGCACCTATTTGCCCACTTCAATGGCGCTTAAGCAAGTGTGTCTGAGTGTCCAAATGTGTGAC 402
QY 301 CCAGCATGGGCTGTGGCGGAGCGGAGGAGTGTCTCCAGGACAGAGGAGCGGCTGTGTGGC 360
Db 403 CCAGCATGGGCTGTGGCGGAGCGGAGGAGTGTCTCCAGGACAGAGGAGCGGCTGTGTGGC 462
QY 361 TGCAGCCAGGCGCACTTCTGATCTGCTCCAGGACGGGACCACTGCGCGCGCTGTGGCGCT 420
Db 463 TGCAGCCAGGCGCACTTCTGATCTGCTCCAGGACGGGACCACTGCGCGCGCTGTGGCGCT 522
QY 421 TACGCCACCTTCCAGCGCGGCGGAGGAGTGTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
Db 523 TACGCCACCTTCCAGCGCGGCGGAGGAGTGTGCAAGAGGAGGACCGAGAGTCAAGACACC 582
QY 481 CTGTGTGAGAACTGCGCGCGGCGGAGCTTCTTCCAAATGGGACCTTGGAGGAATGTGAG 540
Db 583 CTGTGTGAGAACTGCGCGCGGCGGAGCTTCTTCCAAATGGGACCTTGGAGGAATGTGAG 642
QY 541 CACCAGACCAATG 554
Db 643 CACCAGACCAATG 656

RESULT 15

ABX90577

ID ABX90577 standard; cDNA; 1834 BP.

XX ABX90577;

AC ABX90577;

DT 06-MAY-2003 (first entry)

XX Human membrane-bound Herpesvirus Entry Mediator-2 (mhVEM-2) cDNA.

XX Human; ss; Gene; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KV SHVEM1; SHVEM2; SHVEM3; mhVEM2; tumour necrosis factor receptor; TNFR;
KV immune disorder; autoimmune disorder; arthritis; graft rejection;
KV T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KV psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KV rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KV asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KV systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KV cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KV B-cell cancer.

XX Homo sapiens.

OS US2002132297-A1.

XX 19-SEP-2002.

XX 21-AUG-2001; 2001US-00934289.

XX 03-SEP-1998; 98US-00146950.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ;

XX WPI; 2003-255106/25.

XX P-PSDB; ABU0694.

XX New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

XX Claim 2; Fig 7; 79pp; English.

XX The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mhVEM2 (where HVEM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence encodes a TANGO-69 receptor protein

Sequence 1834 BP; 398 A; 555 C; 540 G; 341 T; 0 U; 0 Other;
Query Match 93.2%; Score 550.8; DB 7; Length 1834;
Best Local Similarity 99.8%; Pred. NO. 1.2e-129; Indels 0; Gaps 0;
Matches 552; Conservative 0; Mismatches 2;
1 ATGGAGCCTCTCGAGACTGGGGCTCTCTCTCGAGATCCACCCCGAGAACCGAGCTC 60
103 ATGGAGCCTCTCGAGACTGGGGCTCTCTCTCGAGATCCACCCCGAGAACCGAGCTC 162
61 TTGAGGCTGTGTATCTACCTTCTGGAGCCCTCTAGCCCGAGCTCTGGCG 120
163 TTGAGGCTGTGTATCTACCTTCTGGAGCCCTCTAGCCCGAGCTCTGGCG 222
121 TCCTGCAAGGAGACAGTAGTACCCAGTGGGCTCCAGTGTGCCCCCAAGTGCAGTCCAGGT 180
223 TCCTGCAAGGAGACAGTAGTACCCAGTGGGCTCCAGTGTGCCCCCAAGTGCAGTCCAGGT 282
181 TATCGTGTGAAGAGGCTCTCGGGAGCTGA CGGGCAAGTGTGTGAACCTTGCCTTCA 240
283 TATCGTGTGAAGAGGCTCTCGGGAGCTGACGGGCACAGTGTGTGAACCTTGCCTTCA 342
241 GGCACCTACATTCGCCACCTCAATGGCTAAGCAAGTGTGTGAGTGCCAAATGTGTGAC 300
343 GGCACCTACATTCGCCACCTCAATGGCTAAGCAAGTGTGTGAGTGCCAAATGTGTGAC 402
301 CCAGCCATGGGCTCTGCGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTGCG 360
403 CCAGCCATGGGCTCTGCGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTGCG 462
361 TGCAGCCAGGCCACTTCTGATCTCCAGGACGGGACCACTGCGCCGCGTGC CGCGCT 420
463 TGCAGCCAGGCCACTTCTGATCTCCAGGACGGGACCACTGCGCCGCGTGC CGCGCT 522
421 TAGGCCACTTCAGCCCGGGCCAGAGGCTG CAGAAGGGAGGACCCAGAGTCAAGACACC 480
523 TAGGCCACTTCAGCCCGGGCCAGAGGCTG CAGAAGGGAGGACCCAGAGTCAAGACACC 582
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAG 540
583 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAG 642
541 CACCAAGCAATTG 554
643 CACCAGACCAAGTG 656

Sult No.	Query No.	Score	Match	Length	DB	ID	Description
1	591	100.0	591	3	US-09-146-950-19	Sequence 19, Appl	
2	591	100.0	1596	3	US-09-146-950-17	Sequence 17, Appl	
3	592.6	93.5	4622	3	US-08-508-034-6	Sequence 6, Appl	
4	592.6	93.5	4622	4	US-09-333-279-6	Sequence 6, Appl	
5	592.6	93.5	4622	4	US-09-631-780-6	Sequence 6, Appl	
6	590.8	93.2	1724	3	US-08-509-034-1	Sequence 1, Appl	
7	590.8	93.2	1724	4	US-09-333-279-1	Sequence 1, Appl	
8	590.8	93.2	1724	4	US-09-631-780-1	Sequence 1, Appl	
9	590	93.1	579	3	US-09-146-950-3	Sequence 3, Appl	
10	590	93.1	1929	3	US-09-146-950-1	Sequence 1, Appl	
11	544.4	92.1	1724	5	PCF-US96-12374-1	Sequence 1, Appl	
12	340.2	57.6	976	4	US-09-016-434-937	Sequence 937, Appl	
13	114	19.3	114	3	US-09-146-950-22	Sequence 22, Appl	
14	112.4	19.0	114	3	US-09-146-950-6	Sequence 6, Appl	
15	61.2	10.4	691	1	US-08-266-080B-12	Sequence 12, Appl	
16	61.2	10.4	691	5	PCF-US95-05423-12	Sequence 12, Appl	
17	61.2	10.4	705	4	US-09-326-394-3	Sequence 3, Appl	
18	59.6	10.1	705	4	US-09-580-235-3	Sequence 3, Appl	
19	59.6	10.1	705	4	US-09-580-235-7	Sequence 7, Appl	
20	59.6	10.1	705	4	US-09-580-181-3	Sequence 3, Appl	
21	59.6	10.1	705	4	US-09-580-181-7	Sequence 7, Appl	
22	59.6	10.1	705	4	US-09-103-530-3	Sequence 3, Appl	
23	59.6	10.1	705	4	US-09-103-530-7	Sequence 7, Appl	
24	59.6	10.1	1557	1	US-08-385-259-3	Sequence 3, Appl	
25	59.6	10.1	1557	4	US-09-579-845-2	Sequence 2, Appl	
26	59.6	10.1	1641	1	US-08-385-229-1	Sequence 1, Appl	
27	59.6	10.1	1641	2	US-08-650-000-1	Sequence 1, Appl	

421 TAGCCACCTCCAGCCCGGSCCAGAGGGTGCAGAGGGAGGACCGAGAGTCCAGACACC 480
421 TAGCCACCTCCAGCCCGGSCCAGAGGGTGCAGAGGGAGGACCGAGAGTCCAGACACC 480
481 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
481 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
541 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 591
541 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 591

SULT 2

-09-146-950-17

Sequence 17, Application US/09146950A

Patent No. 6287808

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 09404/057001

CURRENT APPLICATION NUMBER: US/09/146,950A

CURRENT FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 17

LENGTH: 1596

TYPE: DNA

ORGANISM: Homo sapiens

-09-146-950-17

Query Match 100.0%; Score 591; DB 3; Length 1596;

Best Local Similarity 100.0%; Pred. No. 2,6e-147; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACCGACGTC 60
107 ATGAGCCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACCGACGTC 166
61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTAGCCCCAGCTCTGCCG 120
167 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTAGCCCCAGCTCTGCCG 226
121 TCCTCCAAAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCCCAAGTCCAGT 180
227 TCCTCCAAAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCCCAAGTCCAGT 286
181 TATCTGTGAAGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTAACCTGCCCTCA 240
287 TATCTGTGAAGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTAACCTGCCCTCA 346
241 GGCACTACATTCGCCCACTCAATGGCCTAAGCAAGTGTCTGCAGTGCCCAATGTGTGAC 300
347 GGCACTACATTCGCCCACTCAATGGCCTAAGCAAGTGTCTGCAGTGCCCAATGTGTGAC 406
301 CCAGCCATGGGCTCTGGGCGGAGCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGC 360
407 CCAGCCATGGGCTCTGGGCGGAGCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGC 466
361 TGACGCCAGGCACTTCTGCATCTGTCCAGACCGGGACCACTGCGCGCGGTGCGCGCT 420
467 TGACGCCAGGCACTTCTGCATCTGTCCAGACCGGGACCACTGCGCGCGGTGCGCGCT 526
421 TAGGCCACCTCCAGCCCGGCGAGAGGTGTCAGAGGAGGACACCGAGAGTCCAGACACC 480
527 TAGGCCACCTCCAGCCCGGCGAGAGGTGTCAGAGGAGGACACCGAGAGTCCAGACACC 586
481 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
587 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 646

QY 541 CACCAGACCAATTGGCCTAATCATATGTGTGAAAGAGAAAGCAAGGGG 591
Db 647 CACCAGACCAATTGGCCTAATCATATGTGTGAAAGAGAAAGCAAGGGG 697

RESULT 3

US-08-509-024-6

Sequence 6, Application US/08509024B

Patent No. 6281207

GENERAL INFORMATION:

APPLICANT: SPEAR, Patricia G.

APPLICANT: MONTGOMERY, Rebecca I.

TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN

FILE REFERENCE: 0290-1

CURRENT APPLICATION NUMBER: US/08/509,024B

CURRENT FILING DATE: 1995-07-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 4622

TYPE: DNA

ORGANISM: Homo sapiens

US-08-509-024-6

Query Match 93.5%; Score 552.6; DB 3; Length 4622;

Best Local Similarity 98.4%; Pred. No. 5.3e-137;

Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGCCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACCGACGTC 60
64 ATGAGCCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACCGACGTC 123
61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTAGCCCCAGCTCTGCCG 120
124 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTAGCCCCAGCTCTGCCG 183
121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTCCAGT 180
184 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTCCAGT 243
181 TATCTGTGAAGAGGAGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCA 240
244 TATCTGTGAAGAGGAGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCA 303
241 GGCACTACATTCGCCCACTCAATGGCCTAAGCAAGTGTCTGCAGTGCCCAATGTGTGAC 300
304 GGCACTACATTCGCCCACTCAATGGCCTAAGCAAGTGTCTGCAGTGCCCAATGTGTGAC 363
301 CCAGCCATGGGCTCTGGGCGGAGCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGC 360
364 CCAGCCATGGGCTCTGGGCGGAGCGGAACTGTCTCAGGACAGAGAAACCGCTGTGTGC 423
361 TGACGCCAGGCACTTCTGCATCTGTCCAGACCGGGACCACTGCGCGCGGTGCGCGCT 420
424 TGCAGCCAGGCACTTCTGCATCTGTCCAGACCGGGACCACTGCGCGCGGTGCGCGCT 483
421 TACGCCACCTCCAGCCCGGCGCAGAGGCTGCAGAGGAGGACCGAGAGTCCAGACACC 480
484 TACGCCACCTCCAGCCCGGCGCAGAGGCTGCAGAGGAGGACCGAGAGTCCAGACACC 543
481 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
544 CTGTGTGAGAACTGCCCCCGGAGCCTTCTCCCAATGGGACCTGGAGGAATGTGAG 603
541 CACCAGACCAATTGGCCTAATCATATG 567
604 CACCAGACCAATTGGCCTAATCATG 630

RESULT 4

US-09-333-279-6

Sequence 6, Application US/09333279

Patent No. 6303336

GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/09/333,279
 CURRENT FILING DATE: 1999-06-15
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 EQ ID NO 6
 LENGTH: 4622
 TYPE: DNA
 ORGANISM: Homo sapiens
 09-333-279-6

Query Match 93.5%; Score 552.6; DB 4; Length 4622;
 Best Local Similarity 98.4%; Pred. No. 5.3e-137;
 Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 60
 64 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 123
 61 TTGAGGCTGGTGTATCTCACTTTCTGGAGACCCCTGTACGCCCCAGCTCTGCCG 120
 124 TTGAGGCTGGTGTATCTCACTTTCTGGAGACCCCTGTACGCCCCAGCTCTGCCG 183
 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAAGTCCAGGT 180
 184 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAAGTCCAGGT 243
 181 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGCAACAGTGTGTGAACCCCTGCCCTCCA 240
 244 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGCAACAGTGTGTGAACCCCTGCCCTCCA 303
 241 GGCACTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 300
 304 GGCACTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 363
 301 CCAGCCATGGGCTGTGGCGGAGCCGGAACCTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 360
 364 CCAGCCATGGGCTGTGGCGGAGCCGGAACCTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 423
 361 TGCAGCCAGGACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 420
 424 TGCAGCCAGGACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 483
 421 TACGCCACCTCCAGCCCGGCGGAGAGGCTGACAGAGGAGGACCCAGAGAGTCAAGACACC 480
 484 TACGCCACCTCCAGCCCGGCGGAGAGGCTGACAGAGGAGGACCCAGAGAGTCAAGACACC 543
 481 CTGTGTCAAGTGCACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 540
 544 CTGTGTCAAGTGCACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 603

SUIT 5
 -09-631-780-6
 Sequence 6, Application US/09631780
 Patent No. 6573058
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/09/631,780
 CURRENT FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US/08/509,024B
 PRIOR FILING DATE: 1995-07-25

NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 EQ ID NO 6
 LENGTH: 4622
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-631-780-6

Query Match 93.5%; Score 552.6; DB 4; Length 4622;
 Best Local Similarity 98.4%; Pred. No. 5.3e-137;
 Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 60
 64 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 123
 61 TTGAGGCTGGTGTATCTCACTTTCTGGAGACCCCTGTACGCCCCAGCTCTGCCG 120
 124 TTGAGGCTGGTGTATCTCACTTTCTGGAGACCCCTGTACGCCCCAGCTCTGCCG 183
 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAAGTCCAGGT 180
 184 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAAGTCCAGGT 243
 181 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGCAACAGTGTGTGAACCCCTGCCCTCCA 240
 244 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGCAACAGTGTGTGAACCCCTGCCCTCCA 303
 241 GGCACTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 300
 304 GGCACTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 363
 301 CCAGCCATGGGCTGTGGCGGAGCCGGAACCTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 360
 364 CCAGCCATGGGCTGTGGCGGAGCCGGAACCTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 423
 361 TGCAGCCAGGACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 420
 424 TGCAGCCAGGACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 483
 421 TACGCCACCTCCAGCCCGGCGGAGAGGCTGACAGAGGAGGACCCAGAGAGTCAAGACACC 480
 484 TACGCCACCTCCAGCCCGGCGGAGAGGCTGACAGAGGAGGACCCAGAGAGTCAAGACACC 543
 481 CTGTGTCAAGTGCACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 540
 544 CTGTGTCAAGTGCACCTCTCTCATCTCCAGAGCGGGACCACTGCGCGCGCTGCGCGCT 603

RESULT 6
 US-08-509-024-1
 Sequence 1, Application US/08509024B
 Patent No. 6291207
 GENERAL INFORMATION:
 APPLICANT: SPEAR, Patricia G.
 APPLICANT: MONTGOMERY, Rebecca I.
 TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
 FILE REFERENCE: 0290-1
 CURRENT APPLICATION NUMBER: US/08/509,024B
 CURRENT FILING DATE: 1995-07-25
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 EQ ID NO 1
 LENGTH: 1724
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-08-509-024-1

Query Match 93.2%; Score 550.8; DB 3; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.2e-136; Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
294 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
61 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120
354 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 413
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 180
414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 473
181 TATCGTGTGAAGAGGCTCTGGAGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 240
474 TATCGTGTGAAGAGGCTCTGGAGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 533
241 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 300
534 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 593
301 CCAGCCATGGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 360
594 CCAGCCATGGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 653
361 TGCAGCCAGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 420
654 TGCAGCCAGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 713
421 TACGCCACTCCAGCCCGGCGAGCGGAACTGTCTCCAGGACAGGAGTGCAGGACACC 480
714 TACGCCACTCCAGCCCGGCGAGCGGAACTGTCTCCAGGACAGGAGTGCAGGACACC 773
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGAGGAATGTCTAG 540
774 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGAGGAATGTCTAG 833
541 CACCAGACCAATTG 554
834 CACCAGACCAATTG 847

RESULT 7

3-09-333-279-1
Sequence 1, Application US/09333279
Patent No. 6303336
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
S-09-333-279-1

Query Match 93.2%; Score 550.8; DB 4; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
294 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
61 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120

Db QY 354 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 413
QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 180
Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 473
QY 181 TATCGTGTGAAGAGGCTCTGGAGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 240
Db 474 TATCGTGTGAAGAGGCTCTGGAGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 533
QY 241 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 300
Db 534 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 593
QY 301 CCAGCCATGGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 360
Db 594 CCAGCCATGGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 653
QY 361 TGCAGCCAGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 420
Db 654 TGCAGCCAGGCTCTGGAGGAGCTGACGGGACAGTGTGCAAGTGCACAAATGTGTGAC 713
QY 421 TACGCCACTCCAGCCCGGCGAGCGGAACTGTCTCCAGGACAGGAGTGCAGGACACC 480
Db 714 TACGCCACTCCAGCCCGGCGAGCGGAACTGTCTCCAGGACAGGAGTGCAGGACACC 773
QY 481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGAGGAATGTCTAG 540
Db 774 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGAGGAATGTCTAG 833
QY 541 CACCAGACCAATTG 554
Db 834 CACCAGACCAATTG 847

RESULT 8

US-09-631-780-1
Sequence 1, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-631-780-1

Query Match 93.2%; Score 550.8; DB 4; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
Db 294 ATGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
QY 61 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120
Db 354 TTGAGGCTCTCTGGAGACTGGGGCCCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 413
QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 180
Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 473
QY 181 TATCGTGTGAAGAGGCTCTGGAGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 240

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474 TATCGGTGTAAGAGGAGGCTGGGGGAGCTGACGGGCAAGTGTGTGAACCTTGCCTTCCA 533
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAGTGTCTGCAAGTGCCTCAATGTGTGAC 300
534 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAGTGTCTGCAAGTGCCTCAATGTGTGAC 593
301 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 360
594 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 653
361 TGCAGCCAGGCGACTTTCGATCGTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 420
654 TGCAGCCAGGCGACTTTCGATCGTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 713
421 TAGCCCACTCCAGCCCGGGCGAGAGGGTGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGAC 480
714 TAGCCCACTCCAGCCCGGGCGAGAGGGTGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGAC 773
481 CTGTGTCAAGAACTGGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
774 CTGTGTCAAGAACTGGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 833
541 CACCAGACCAATGTG 554
834 CACCAGACCAATGTG 847

JUL 9
-09-146-950-3
Sequence 3, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 579
TYPE: DNA
ORGANISM: Homo sapiens
-09-146-950-3

Query Match 93.1%; Score 550; DB 3; Length 579;
Best Local Similarity 99.1%; Pred. No. 1.4e-136;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
61 TTGAGGCTGGTGTATCTACCTTCTGGAGCCCTCTGCTAGCCGCCAGCTCTGCG 120
61 TTGAGGCTGGTGTATCTACCTTCTGGAGCCCTCTGCTAGCCGCCAGCTCTGCG 120
121 TCCTGCAAGGAGGACGAGTACCAGTGGGTCTGCGGCTGCTGCGGCTGCTGCG 180
121 TCCTGCAAGGAGGACGAGTACCAGTGGGTCTGCGGCTGCTGCGGCTGCTGCG 180
181 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCA 240
181 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCA 240
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTGCCTTGTGAC 300
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTGCCTTGTGAC 300
301 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 360
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301 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 360
361 TGCAGCCAGGCGACTTTCGATCGTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 420
361 TGCAGCCAGGCGACTTTCGATCGTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 420
421 TACGCCACTCCAGCCCGGGCGAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGACACC 480
421 TACGCCACTCCAGCCCGGGCGAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGACACC 480
481 CTGTGTCAAGAACTGGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
481 CTGTGTCAAGAACTGGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
541 CACCAGACCAATGTGCGCT 558
541 CACCAGACCAATGTGCGCT 558

RESULT 10
US-09-146-950-1
Sequence 1, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)...(875)
US-09-146-950-1

Query Match 93.1%; Score 550; DB 3; Length 1929;
Best Local Similarity 99.1%; Pred. No. 2e-136;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
DB 297 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 356
QY 61 TTGAGGCTGGTGTATCTACCTTCTGGAGCCCTCTGCTAGCCGCCAGCTCTGCG 120
DB 357 TTGAGGCTGGTGTATCTACCTTCTGGAGCCCTCTGCTAGCCGCCAGCTCTGCG 416
QY 121 TCCTGCAAGGAGGACGAGTACCAGTGGGTCTGCGGCTGCTGCGGCTGCTGCG 180
DB 417 TCCTGCAAGGAGGACGAGTACCAGTGGGTCTGCGGCTGCTGCGGCTGCTGCG 476
QY 181 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCA 240
DB 477 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCA 536
QY 241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTGCCTTGTGAC 300
DB 537 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTGCCTTGTGAC 596
QY 301 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 360
DB 597 CCAGCCATGGGCTTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAAACGCGGTGTGTGGC 656
QY 361 TGCAGCCAGGCGACTTTCGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 420
DB 657 TGCAGCCAGGCGACTTTCGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 716
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Y 421 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 480
b 717 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 776
Y 481 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 540
b 777 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 836
Y 541 CACCAGACCAATTGGCCT 558
b 837 CACCAGACCAACCGAGCT 854

RESULT 11

CT-US96-12374-1

Sequence 1, Application PC/TUS9612374

GENERAL INFORMATION:

APPLICANT: Northwestern University

TITLE OF INVENTION: Herpes Virus Entry Mediator

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.

STREET: 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/12374

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Northrup, Thomas E.

REGISTRATION NUMBER: 33,268

REFERENCE/DOCKET NUMBER: NOR3446P020PC

TELEPHONE: (312) 616-5400

TELEFAX: (312) 616-5460

TELEX: --

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1724 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 294..1145

FEATURE:

NAME/KEY: mat peptide

LOCATION: 294..1142

CT-US96-12374-1

Query Match 92.1%; Score 544.4; DB 5; Length 1724;
Best Local Similarity 98.9%; Pred. No. 5.8e-135;
Matches 548; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2Y 1 ATGAGGCTCTGAGAGTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAGCCGACGTC 60
b 294 ATGAGGCTCTGAGAGTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAGCCGACGTC 353
2Y 61 TTGAGGCTGGTGTATCTACACTTTCTGGAGCCCCCTGTACGCCAGCTTGGCG 120
b 354 TTGAGGCTGGTGTATCTACACTTTCTGGAGCCCCCTGTACGCCAGCTTGGCG 413
2Y 121 TCCTCAAGGAGGAGGAGTACCCAGTGGGCTCCGAGTGGCTGCCCAAGTCAGTCCAGT 180

Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGGCTCCCAAGTCAGTCCAGGT 473
QY 181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
Db 474 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
QY 241 GGCACCTACATTGGCCCACTCAATGGGCTAAGCAAGTGTGTGAGTGCCAAATGTGTGAC 300
Db 534 GGCACCTACATTGGCCCACTCAATGGGCTAAGCAAGTGTGTGAGTGCCAAATGTGTGAC 593
QY 301 CCAGCCATGGGCTCGGGGAGCGGAGCTGTCCAGGACAGAGAACCGCTGTGTGGC 360
Db 594 CCAGCCATGGGCTCGGGGAGCGGAGCTGTCCAGGACAGAGAACCGCTGTGTGGC 653
QY 361 TGCAGCCAGGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGGCTGCGCGCT 420
Db 654 TGCAGCCAGGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGGCTGCGCGCT 713
QY 421 TACGCCACTTCAGCCCGGGCCAGAGGCTGCAAGGAGGACCGAGAGTCAGGACACC 480
Db 714 TACGCCACTTCAGCCCGGGCCAGAGGCTGCAAGGAGGACCGAGAGTCAGGACACC 773
QY 481 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 540
Db 774 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAC 833
QY 541 CACCAGACCAATTG 554
Db 834 CACCAGACCAAGTG 847

RESULT 12

US-09-016-434-937

; Sequence 937, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 937:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 976 base pairs

; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MYOMNOT01
CLONE: 778805
09-016-434-937

Query Match 57.6%; Score 340.2; DB 4; Length 976;
 Best Local Similarity 83.2%; Pred. No. 5.7e-81;
 Matches 462; Conservative 0; Mismatches 3; Indels 90; Gaps 3;

1 ATGGAGCCTCTTGAGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCAAGAACCGACGTC 60
121 ATGGAGCCTCTTGAGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCAAGAACCGACGTC 180	
61 TTGAGGCTGGTGTCTATCTCACCTTTCTGGGAGCCCTCTGTGTAGGCCCCAGCTCTGGCG 120	
181 TTGAGGCTGGTGTCTATCTCACCTTTCTGGGAGCCCTCTGTGTAGGCCCCAGCTCTGGCG 240	
121 TCTCGCAAGGAGGACGATAGCCAGTGGGCTCCGAGTGTGCCCCCAAGTGCAGTCCAGGT 180	
241 TCTCGCAAGGAGGACGATAGCCAGTGGGCTCCGAGTGTGCCCCCAAGTGCAGTCCAGGT 300	
181 TATCTGTGAAGAGGCGCTGCGGAGCTGCGGGCACAGTGTGTGAACCTTGCCCTCA 240	
301 TA---TGTGAAGAGGCGCTGCGGAGCTGACGGCACAGTGTGTGAACCTTGCCCTCA 357	
241 GGCACCTACATTGCCACCTCAATGGGCTTAAGCAAGTGTCTGCAGTGCCTCAAAATGTGTAC 300	
358 GGCACCTACATTGCCACCTCAATGGGCTTAAGCAAGTGTCTGCAGTGCCTCAAAATGTGTAC 417	
301 CCAGCCATGGGCTCGGCGCGAGCGGAACTGTCTCCAGGACAGAGAACCGGTGTGTGGC 360	
418 ----- 417	
361 TGAAGCCAGGCCACTTCTGATCTGTCCAGAGCGGGACCACTGCGCCCGGTGCGCGGT 420	
418 ----- 451	
421 TAGCGACCTTCAGCCCGGCGAGAGGGTGCAGAGGGAGGACACAGAGTCCAGAGCACCC 480	
452 TAGCCACCTTCAGCCCGGCGAGAGGGTGCAGAGGGAGGACACAGAGTCCAGAGCACCC 511	
481 CTGTGTCAAACTGCCCCCGGGAGCC--TTCTCTCCCAATGGGACCCCTGGAGGAATGTCA 539	
512 CTGTGTCAAACTGCCCCCGGGAGCCTTTCTCTCCCAATGGGAGCCCTGGAGGAATGTCA 571	
540 GCACCGAGACCAATTG 554	
572 GCACCGAGACCAAGTG 586	

3ULT 13
 .09-146-950-22
 Sequence 22, Application US/09146950A
 Patent No. 6287808
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J.
 TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
 FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 09404/057001
 CURRENT APPLICATION NUMBER: US/09/146,950A
 CURRENT FILING DATE: 1998-09-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 22
 LENGTH: 114
 TYPE: DNA
 ORGANISM: Homo sapiens
 -09-146-950-22

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Query Match      19.3%; Score 114; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
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	Matches	114;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGAGGCTCTGAGAGCTGGGGGCTCTCCTCGAGATCCACCCGAGAACCGAGTC	60							
DB	1	ATGAGGCTCTGAGAGCTGGGGGCTCTCCTCGAGATCCACCCGAGAACCGAGTC	60							
QY	61	TTGAGGCTGCTGTATCTCACTTTCTGGAGGCCCTGCTAGGCCGAGCT	114							
DB	61	TTGAGGCTGCTGTATCTCACTTTCTGGAGGCCCTGCTAGGCCGAGCT	114							

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RESULT 14
US-09-146-950-6
; Sequence 6, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-950-6

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Query Match	19.0%;	Score 112.4;	DB 3;	Length 114;
Best Local Similarity	99.1%;	Prod. No. 6.3e-21;		
Matches 113;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	ATGGAGCCCTCTCGAGACTCGGGGCTCTCTCTCGAGATCCACCCCGAGACCGAGCTC	60
Db	1	ATGGAGCCCTCTCGAGACTCGGGGCTCTCTCTCGAGATCCACCCCGAGACCGAGCTC	60
QY	61	TTGAGCTGTGGTGTGATCTCACTTTCTGGGAGCCCCCTGTAGCCCCCAAGCT	114
Db	61	TTGAGCTGTGGTGTGATCTCACTTTCTGGGAGCCCCCTGTAGCCCCCAAGCT	114

RESULT 15
US-08-266-080B-12
Sequence 12, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Iale
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
S-08-266-080B-12

Query Match: 10.4%; Score 61.2; DB 1; Length 691;
Best Local Similarity 50.0%; Pred. No. 3.8e-07;
Matches 181; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

y	156	GTGCTGCCCCCAAGTCAGTCAGGTTATCGTGTGAAGGAGGCTCGCGGGAGCTGACGGG	215
c	228	GTGCTGCACCAAGTGTCTCGCGGGCCACATGCAAAAGTCTTCTGTACCAAGACCTCGGA	287
y	216	CACAGTGTGTGAACCTGCGCTCCAGGCACTTACATTCGCCCACTCAATGGCCTTAAGCAA	275
b	288	CACCGTGTGTGACTCTCTGTGAGGACAGCACATACACCCAGCTCTGGAAGTGGGTTCGCCA	347
y	276	GTGCTGTGAGTCCCAATGTGTGACCCAGCCATGGGCTCGCGGAGCCGGAACCTGCTC	335
c	348	GTCTTGAGCTGTGG---CTCCCGTGTAGTCTTACCAGGTGAAACTCAAGCCTGCAC	404
y	336	CAGGACAGAGAACCGCGTGTGTGGCTGCAGCCCGAGGCCACTTCTGCATCTCTCCAGGACGG	395
b	405	TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGCTACTGCGCGCTGAGCAAGCA	464
y	396	GGACCACTGGCGCGGTGCGCGCTTACGCCACTTCAGCCCGGGCCAGAGGGTGCAGAA	455
b	465	GGAGGGGTGCGGCTGTGCGGCCCTGCGCAAGTGGTGTGCAAGCCCTGTGCCCCGGGAGGTTCTCCAA	524
y	456	GGAGGCACTCGAGAGTTCAGGACCACTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCC	515
b	525	ACCAGGAATGAAACATCAGAGTGGTGTGCAAGCCCTGTGCCCCGGGAGGTTCTCTCCAA	584
y	516	CA 517	
b	585	CA 586	

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ob time : 89 secs

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nucleic - nucleic search, using sw model

n on: June 10, 2004, 09:41:11 ; Search time 350 seconds
(without alignments)
7707.497 Million cell updates/sec

file: US-09-934-289A-19
rfect score: 591
quence: 1 atggagcctctggagactg.....aaagaagaagcaagggg 591

oring table: IDENTITY_NUC
Gapex 10.0 , Capext 1.0

arched: 2998549 seqs, 2282253817 residues
tal number of hits satisfying chosen parameters: 5997098

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
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9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq.*
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15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
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18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	591	100.0	591	9	US-09-934-289A-19	Sequence 19, Appl
2	591	100.0	1596	9	US-09-934-289A-17	Sequence 17, Appl
3	522.6	93.5	4622	9	US-09-924-231-6	Sequence 6, Appl
4	550.8	93.2	831	9	US-09-934-289A-43	Sequence 43, Appl
5	550.8	93.2	1724	9	US-09-924-231-1	Sequence 1, Appl
6	550.8	93.2	1724	9	US-09-934-289A-14	Sequence 14, Appl
7	550.8	93.2	1724	16	US-10-369-300-1	Sequence 1, Appl
8	550.8	93.2	1834	9	US-09-934-289A-41	Sequence 41, Appl
9	550	93.1	579	9	US-09-934-289A-3	Sequence 3, Appl
10	550	93.1	1929	9	US-09-934-289A-1	Sequence 1, Appl
11	548.4	92.8	558	9	US-09-934-289A-31	Sequence 31, Appl
12	548.4	92.8	2313	9	US-09-934-289A-29	Sequence 29, Appl
13	547.6	92.7	1704	14	US-10-020-787-1	Sequence 1, Appl
14	340.2	57.6	976	16	US-10-305-720-937	Sequence 937, App

15	259.6	43.9	1082	16	US-10-369-300-3	Sequence 3, Appl
16	233.8	39.6	447	10	US-09-918-995-3536	Sequence 3536, Ap
17	168.8	28.6	350	9	US-09-783-590-11975	Sequence 11975, A
18	126	21.3	126	9	US-09-934-289A-11	Sequence 11, Appl
19	126	21.3	126	9	US-09-934-289A-12	Sequence 12, Appl
20	126	21.3	126	9	US-09-934-289A-27	Sequence 27, Appl
21	126	21.3	126	9	US-09-934-289A-28	Sequence 28, Appl
22	126	21.3	126	9	US-09-934-289A-39	Sequence 39, Appl
23	126	21.3	126	9	US-09-934-289A-40	Sequence 40, Appl
24	126	21.3	126	9	US-09-934-289A-53	Sequence 53, Appl
25	126	21.3	126	9	US-09-934-289A-54	Sequence 54, Appl
26	110.8	18.7	114	9	US-09-934-289A-6	Sequence 6, Appl
27	110.8	18.7	114	9	US-09-934-289A-22	Sequence 22, Appl
28	110.8	18.7	114	9	US-09-934-289A-34	Sequence 34, Appl
29	110.8	18.7	114	9	US-09-934-289A-46	Sequence 46, Appl
30	105	17.8	105	9	US-09-934-289A-10	Sequence 10, Appl
31	105	17.8	105	9	US-09-934-289A-26	Sequence 26, Appl
32	105	17.8	105	9	US-09-934-289A-38	Sequence 38, Appl
33	105	17.8	105	9	US-09-934-289A-52	Sequence 52, Appl
34	62.4	10.6	1968	16	US-10-262-445-122	Sequence 122, App
35	62.4	10.6	1982	9	US-09-907-372-2	Sequence 2, Appl
36	62.4	10.6	1982	10	US-09-917-372-2	Sequence 2, Appl
37	62.4	10.6	2105	16	US-10-369-300-16	Sequence 16, Appl
38	62.4	10.6	2136	9	US-09-962-436-262	Sequence 262, App
39	62.4	10.6	2136	9	US-09-880-107-2135	Sequence 2135, Ap
40	62.4	10.6	2136	9	US-09-954-531-1348	Sequence 1348, Ap
41	62.4	10.6	2136	10	US-09-960-706-634	Sequence 634, App
42	62.4	10.6	2136	10	US-09-873-319-397	Sequence 397, App
43	62.4	10.6	2136	13	US-10-342-887-759	Sequence 759, App
44	62.4	10.6	2136	13	US-10-172-118-759	Sequence 759, App
45	62.4	10.6	2136	16	US-10-159-563-411	Sequence 411, App

ALIGNMENTS

RESULT 1
US-09-934-289A-19
; Sequence 19, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB108-061CPC1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(591)
US-09-934-289A-19

Query Match 100.0%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 9.1e-167; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0;
Qy 1 ATGGAGCCTCTGGAGACTGGGGCCCTCTCTCGAGATCCACCCAGAACCCGACGTC 60
Db 1 ATGGAGCCTCTGGAGACTGGGGCCCTCTCTCGAGATCCACCCAGAACCCGACGTC 60
Qy 61 TTGAGGTGTGTGTATCTACCTTCTTGGAGCCCCCTGTAGCCCCCAGCTTCGCG 120

61 TTGAGGCTGGTGTCTATCTCACTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
121 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGATGCTGCCCCCAAGTGCATCCAGGT 180
121 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGATGCTGCCCCCAAGTGCATCCAGGT 180
181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
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241 GGCACTACATTGCCCACTCAATGGCCCTAAGCAAGTGTGTGCAAGTGCCTCAATGTGAC 300
241 GGCACTACATTGCCCACTCAATGGCCCTAAGCAAGTGTGTGCAAGTGCCTCAATGTGAC 300
301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACCGCTGTGGC 360
301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACCGCTGTGGC 360
361 TCGAGCCAGGCACTTCTGATCGTCCAGGACGGGACCACTGCGCGGCTCCCGCT 420
361 TCGAGCCAGGCACTTCTGATCGTCCAGGACGGGACCACTGCGCGGCTCCCGCT 420
421 TAGGCACTCCAGCGCGGCGAGGGTGCAGAGGGACCGAGAGTCAGGACACC 480
421 TAGGCACTCCAGCGCGGCGAGGGTGCAGAGGGACCGAGAGTCAGGACACC 480
481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCCCAATGGGACCTCGGAGGAATGTGAG 540
481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCCCAATGGGACCTCGGAGGAATGTGAG 540
541 CACGAGCAATGGCCCTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591
541 CACGAGCAATGGCCCTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591

RESULT 2

3-09-934-289A-17
Sequence 17, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CPI(N1M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 1596
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (107)...(697)
S-09-934-289A-17

Query Match 100.0%; Score 591; DB 9; Length 1596;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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61 TTGAGGCTGGTGTATCTCACTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
167 TTGAGGCTGGTGTATCTCACTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 226

QY 121 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGATGCTGCCCCCAAGTGCATCCAGGT 180
Db 227 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGATGCTGCCCCCAAGTGCATCCAGGT 286
QY 181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
Db 287 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 346
QY 241 GGCACTACATTGCCCACTCAATGGCCCTAAGCAAGTGTGTGCAAGTGCCTCAATGTGAC 300
Db 347 GGCACTACATTGCCCACTCAATGGCCCTAAGCAAGTGTGTGCAAGTGCCTCAATGTGAC 406
QY 301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACCGCTGTGGC 360
Db 407 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACCGCTGTGGC 466
QY 361 TCGAGCCAGGCACTTCTGATCGTCCAGGACGGGACCACTGCGCGGCTCCCGCT 420
Db 467 TCGAGCCAGGCACTTCTGATCGTCCAGGACGGGACCACTGCGCGGCTCCCGCT 526
QY 421 TACGCACTCCAGCGCGGCGAGGGTGCAGAGGGACCGAGAGTCAGGACACC 480
Db 527 TACGCACTCCAGCGCGGCGAGGGTGCAGAGGGACCGAGAGTCAGGACACC 586
QY 481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCCCAATGGGACCTCGGAGGAATGTGAG 540
Db 587 CTGTGTGAGAACTGCCCCCGGGACCTTCTCCCAATGGGACCTCGGAGGAATGTGAG 646
QY 541 CACGAGCAATGGCCCTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591
Db 647 CACGAGCAATGGCCCTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 697

RESULT 3

US-09-924-231-6
Sequence 6, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
TITLE OF INVENTION: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4622
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-231-6

Query Match 93.5%; Score 552.6; DB 9; Length 4622;
Best Local Similarity 98.4%; Pred. No. 3.7e-155;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
1 ATGAGCCCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGAGTC 60
64 ATGAGCCCTCTGGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGAGTC 123
61 TTGAGGCTGGTGTATCTCACTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
124 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 183
121 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGTGTGCTGCCCAAGTGCATCCAGGT 180
184 TCTTCGAAGGAGGAGAGTACCCAGTGGGCTCCAGTGTGCTGCCCAAGTGCATCCAGGT 243
181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240

244 TATCGTGTGAAGAGCGCTCGGGAGCTGAGGGGACAGTGTGTGAACCTGCCCTCCA 303
241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 300
304 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 363
301 CCAGCCATGGGCTCGGGGAGCGGAGCTGCTCCAGGACAGAGAACGCGTGTGTGGC 360
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541 CACGACCAATGGCTTATCATATG 567
604 CACGACCAATGGCTTATCATATG 630

JULT 4

09-934-289A-43
Sequence 43, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Buefield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061P1C1N1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 43
LENGTH: 831
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(831)
-09-934-289A-43

Query Match 93.2%; Score 550.8; DB 9; Length 831;
Best Local Similarity 99.6%; Pred. No. 1e-154;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
61 TTGAGCTGTGTGTATCTACCTTCTGGGAGCCCTGCTAGCCCGAGCTGCGG 120
61 TTGAGCTGTGTGTATCTACCTTCTGGGAGCCCTGCTAGCCCGAGCTGCGG 120
121 TCCTGCAAGGAGGACAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
121 TCCTGCAAGGAGGACAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
181 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
181 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240

241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 300
241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 300
301 CCAGCCATGGGCTCGGGGAGCGGAACTGTCTCCAGGACAGAGAACGCGTGTGTGGC 360
301 CCAGCCATGGGCTCGGGGAGCGGAACTGTCTCCAGGACAGAGAACGCGTGTGTGGC 360
361 TGCAGCCAGGCACTTCTGATCTGCTCCAGGACGCGGACCTGCGCGCTGCGCGCT 420
361 TGCAGCCAGGCACTTCTGATCTGCTCCAGGACGCGGACCTGCGCGCTGCGCGCT 420
421 TACGCACTCTCAGCCCGGGGACAGAGGCTGACAGAGGAGGACCGAGAGTTCAGGACAC 480
421 TACGCACTCTCAGCCCGGGGACAGAGGCTGACAGAGGAGGACCGAGAGTTCAGGACAC 480
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAC 540
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAC 540
541 CACGACCAATGG 554
541 CACGACCAATGG 554

RESULT 5

US-09-924-231-1
Sequence 1, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-231-1

Query Match 93.2%; Score 550.8; DB 9; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1e-154;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
294 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 353
61 TTGAGCTGTGTGTATCTACCTTCTGGGAGCCCTGCTAGCCCGAGCTGTGCGG 120
354 TTGAGCTGTGTGTATCTACCTTCTGGGAGCCCTGCTAGCCCGAGCTGTGCGG 413
121 TCCTGCAAGGAGGACAGTACCGAGTGGCTCCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
414 TCCTGCAAGGAGGACAGTACCGAGTGGCTCCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 473
181 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
474 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 300
534 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGAC 593
301 CCAGCCATGGGCTGCGGGAGCGGAGCTGCTCCAGGACAGAGAACGCGTGTGTGCGC 360

b 594 CCAGCCATGGGCTCGCGCGAGCGGAACCTCTCCAGGACAGAGAACGCCGTGTGTGGC 653
y 361 TGCAGCCAGGCACTTCTGATCTCCAGACGGGACCACTGGCGCGGTGCGCGCT 420
b 654 TGCAGCCAGGCACTTCTGATCTCCAGACGGGACCACTGGCGCGGTGCGCGCT 713
y 421 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 480
b 714 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 773
y 481 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTGGAGGAATGTGAG 540
b 774 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTGGAGGAATGTGAG 833
y 541 CACCAGACCAATTG 554
b 834 CACCAGACCAAGTG 847

RESULT 6

S-09-934-289A-14

Sequence 14, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MBIO98-061P1CN1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 1724

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (294)...(1142)

S-09-934-289A-14

Query Match 93.2%; Score 550.8; DB 9; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.1e-154;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
b 294 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 353
y 61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCGCCAGCTCTGCCG 120
b 354 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCGCCAGCTCTGCCG 413
y 121 TCTTCAAGGAGGACGAGTACCACTGGGCTCCAGTGGCTCCAGTGGCTCCAGTGGCTCCAGT 180
b 414 TCTTCAAGGAGGACGAGTACCACTGGGCTCCAGTGGCTCCAGTGGCTCCAGTGGCTCCAGT 473
y 181 TATCGTGTGAAGAGGCTCGCGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
b 474 TATCGTGTGAAGAGGCTCGCGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
y 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
b 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 593
y 301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 360
b 594 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 653

RESULT 7

US-10-369-300-1

Sequence 1, Application US/10369300

Publication No. US2003021542A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher

APPLICANT: Hancock, Wayne

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF

TITLE OF INVENTION: IMMUNE

TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY

FILE REFERENCE: 7853-255

CURRENT APPLICATION NUMBER: US/10/369,300

CURRENT FILING DATE: 2003-02-19

PRIOR APPLICATION NUMBER: 60/358,463

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1724

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (294)..(1145)

OTHER INFORMATION:

US-10-369-300-1

Query Match 93.2%; Score 550.8; DB 16; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.1e-154;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
b 294 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 353
y 61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGCTAGGCCCGAGCTCTGCCG 120
b 354 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTGCTAGGCCCGAGCTCTGCCG 413
y 121 TCTTCAAGGAGGACGAGTACCACTGGGCTCCAGTGGCTCCAGTGGCTCCAGTGGCTCCAGT 180
b 414 TCTTCAAGGAGGACGAGTACCACTGGGCTCCAGTGGCTCCAGTGGCTCCAGTGGCTCCAGT 473
y 181 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
b 474 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
y 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
b 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 593
y 301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 360
b 594 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 653

361 TGCAGCCCGGCGGCTTCTGATCTGTCAGAGCGGGACCACTGGCGCGCTGCGGCGCT 420
654 TGCAGCCCGGCGGCTTCTGATCTGTCAGAGCGGGACCACTGGCGCGCTGCGGCGCT 713
421 TAGCGCCACCTCCAGCCCGGCGGCTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
714 TAGCGCCACCTCCAGCCCGGCGGCTGCAAGAGGAGGACCGAGAGTCAAGACACC 773
481 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCCCAATGGAGACCTTGAGGAATGTGAG 540
774 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCCCAATGGAGACCTTGAGGAATGTGAG 833
541 CACGAGACCAATTG 554
834 CACGAGACCAAGTG 847

RESULT 8

US-09-934-289A-41

Sequence 41, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MBIO98-061CPICN1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 41

LENGTH: 1834

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (103)....(933)

US-09-934-289A-41

Query Match

Best Local Similarity 99.6%; Score 550.8; DB 9; Length 1834;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGACGTC 60
103 ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGACGTC 162
61 TTGAGGCTGTGTGTATCTACCTTTCTGGAGGCCCCCTGTAGCCCCAGCTCTGCG 120
163 TTGAGGCTGTGTGTATCTACCTTTCTGGAGGCCCCCTGTAGCCCCAGCTCTGCG 222
121 TCCTGCAAGAGGACGAGTACCCAGTGGGCTCCAGTGTGCCCCAGTGCAGTCCAGT 180
223 TCCTGCAAGAGGACGAGTACCCAGTGGGCTCCAGTGTGCCCCAGTGCAGTCCAGT 282
181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGAACCCCTGCCCTCCA 240
283 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGAACCCCTGCCCTCCA 342
241 GGCACTTACATTGGCCACCTCAATGGCTAAGCAAGTGTCTGAGTGCCTCAATGTGTAC 300
343 GGCACTTACATTGGCCACCTCAATGGCTAAGCAAGTGTCTGAGTGCCTCAATGTGTAC 402
301 CCAGCCATGGGCTCTGGCGAGCGGAACTGCTCCAGGACAGAGAACCCGCTGTGTGC 360
403 CCAGCCATGGGCTCTGGCGAGCGGAACTGCTCCAGGACAGAGAACCCGCTGTGTGC 462
361 TGCAGCCCGGCGGCTTCTGATCTGTCAGAGCGGGACCACTGGCGCGCTGCGGCGCT 420

Db 463 TGCAGCCCGGCGGCTTCTGATCTGTCAGAGCGGGACCACTGGCGCGCTGCGGCGCT 522
QY 421 TAGCGCCACCTCCAGCCCGGCGGCTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
Db 523 TAGCGCCACCTCCAGCCCGGCGGCTGCAAGAGGAGGACCGAGAGTCAAGACACC 582
QY 481 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCCCAATGGAGACCTTGAGGAATGTGAG 540
Db 583 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCCAATGGAGACCTTGAGGAATGTGAG 642
QY 541 CACGAGACCAATTG 554
Db 643 CACGAGACCAAGTG 656

RESULT 9

US-09-934-289A-3

Sequence 3, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MBIO98-061CPICN1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 579

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)....(579)

US-09-934-289A-3

Query Match

Best Local Similarity 99.1%; Score 550; DB 9; Length 579;

Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGACGTC 60
Db 1 ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGACGTC 60
QY 61 TTGAGGCTGTGTGTATCTACCTTTCTGGAGGCCCCCTGTAGCCCCAGCTCTGCG 120
Db 61 TTGAGGCTGTGTGTATCTACCTTTCTGGAGGCCCCCTGTAGCCCCAGCTCTGCG 120
QY 121 TCCTGCAAGAGGACGAGTACCCAGTGGGCTCCAGTGTGCCCCAGTGCAGTCCAGT 180
Db 121 TCCTGCAAGAGGACGAGTACCCAGTGGGCTCCAGTGTGCCCCAGTGCAGTCCAGT 180
QY 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGAACCCCTGCCCTCCA 240
Db 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGAACCCCTGCCCTCCA 240
QY 241 GGCACTTACATTGGCCACCTCAATGGCTAAGCAAGTGTCTGAGTGCCTCAATGTGTAC 300
Db 241 GGCACTTACATTGGCCACCTCAATGGCTAAGCAAGTGTCTGAGTGCCTCAATGTGTAC 300
QY 301 CCAGCCATGGGCTCTGGCGAGCGGAACTGCTCCAGGACAGAGAACCCGCTGTGTGC 360
Db 301 CCAGCCATGGGCTCTGGCGAGCGGAACTGCTCCAGGACAGAGAACCCGCTGTGTGC 360
QY 361 TGCAGCCCGGCGGCTTCTGATCTGTCAGAGCGGGACCACTGGCGCGCTGCGGCGCT 420

361 TGCAGCCAGGCGCACTTCTGCATCGTCCAGACGGGACCACTGCGCGCGTGCAGGCT 420
421 TAGCGCACTCCAGCCCGGCGGACAGAGGTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
421 TAGCGCACTCCAGCCCGGCGGACAGAGGTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
481 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
481 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
541 CACCAGACCAATGGGCT 558
541 CACCAGACCAACCGAGCT 558

35ULT 10
3-09-934-289A-1
Sequence 1, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CPI.CNI (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)...(875)
3-09-934-289A-1

Query Match 93.1%; Score 550; DB 9; Length 1929;
Best Local Similarity 99.1%; Pred. No. 2e-154;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAAGCCGAGTC 60
297 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAAGCCGAGTC 356
61 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCTCTGCTACGCCCGGCTCTGCG 120
357 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCTCTGCTACGCCCGGCTCTGCG 416
121 TCCTCAAGAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCGGACCGAGTCCAGGT 180
417 TCCTCAAGAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCGGACCGAGTCCAGGT 476
181 TATCTGTGAAGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCGCTCCA 240
477 TATCTGTGAAGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCGCTCCA 536
241 GGCACCTACATTGCCCACTCAATGGCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
537 GGCACCTACATTGCCCACTCAATGGCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 596
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
597 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 656
361 TCAGCCAGGCGCACTTCTGATGCTCCAGACGGGACCACTGCGCGGCTGCGCGCT 420
657 TCAGCCAGGCGCACTTCTGATGCTCCAGACGGGACCACTGCGCGGCTGCGCGCT 716

QY 421 TACGCACTCCAGCCCGGCGGACAGAGGTGCAAGAGGAGGACCGAGAGTCAAGACACC 480
DB 717 TACGCACTCCAGCCCGGCGGACAGAGGTGCAAGAGGAGGACCGAGAGTCAAGACACC 776
QY 481 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
DB 777 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 836
QY 541 CACCAGACCAATGGGCT 558
DB 837 CACCAGACCAACCGAGCT 854

RESULT 11
US-09-934-289A-31
Sequence 31, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CPI.CNI (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(558)
US-09-934-289A-31

Query Match 92.8%; Score 548.4; DB 9; Length 558;
Best Local Similarity 98.9%; Pred. No. 5e-154;
Matches 552; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAAGCCGAGTC 60
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAAGCCGAGTC 60
61 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCTCTGCTACGCCCGGCTCTGCGG 120
61 TCGAGGCTGGTCTATCTACCTTTCTGGAGCCCTCTGCTACGCCCGGCTCTGCGG 120
121 TCCTCAAGAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCGGACCGAGTCCAGGT 180
121 TCCTCAAGAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCGGACCGAGTCCAGGT 180
181 TATCTGTGAAGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCGCTCCA 240
181 TATCTGTGAAGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCGCTCCA 240
241 GGCACCTACATTGCCCACTCAATGGCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
241 GGCACCTACATTGCCCACTCAATGGCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
361 TCAGCCAGGCGCACTTCTGATGCTCCAGACGGGACCACTGCGCGGCTGCGCGCT 420
361 TCGAGCCAGGCGCACTTCTGATGCTCCAGACGGGACCACTGCGCGGCTGCGCGCT 420

421 TAGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAGGGAGGAGGACCGAGAGTCAGACACC 480
421 TAGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAGGGAGGAGGACCGAGAGTCAGACACC 480
481 CTGTGTCAAGTGCAGCCCGGGGACCTTCTCTCCCAATGGAGACCTCGAGGAATGTGAG 540
481 CTGTGTCAAGTGCAGCCCGGGGACCTTCTCTCCCAATGGAGACCTCGAGGAATGTGAG 540
541 CACCAGACCAATTTGGCCT 558
541 CACCAGACCAAAAGGCT 558

JUL 12

-09-934-289A-29

Sequence 29, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: ME1098-061CP1CM1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 2313

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (85)...(642)

-09-934-289A-29

Query Match 92.8%; Score 548.4; DB 9; Length 2313;
Best Local Similarity 98.9%; Pred. No. 6.1e-154;
Matches 552; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 60
85 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 144
61 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTCTGTACGCCCGAGCTCTGCCG 120
145 TCGAGGCTGGTGTATCTCACTTCTGGAGCCCTCTGTACGCCCGAGCTCTGCCG 204
121 TCTGCAAGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCCAGGT 180
205 TCTGCAAGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCCAGGT 264
181 TATCTGTCAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 240
265 TATCTGTCAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 324
241 GGCACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCMAATGTGAC 300
325 GGCACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTGCMAATGTGAC 384
301 CCAGCCATGGGCTTGGCGGAGCGGACTGCTCCAGGACAGAGAACCGGTGTGGC 360
385 CCAGCCATGGGCTTGGCGGAGCGGACTGCTCCAGGACAGAGAACCGGTGTGGC 444
361 TGAGGCCAGGCGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 420
445 TGAGGCCAGGCGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 504
421 TAGGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 480

Db 505 TAGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAGGGAGGAGGACCGAGAGTCAGACACC 564
QY 481 CTGTGTCAAGTGCAGCCCGGGGACCTTCTCTCCCAATGGAGACCTCGAGGAATGTGAG 540
Db 565 CTGTGTCAAGTGCAGCCCGGGGACCTTCTCTCCCAATGGAGACCTCGAGGAATGTGAG 624
QY 541 CACCAGACCAATTTGGCCT 558
Db 625 CACCAGACCAAAAGGCT 642

RESULT 13

US-10-020-787-1

Sequence 1, Application US/10020787

Publication No. US20020102258A1

GENERAL INFORMATION:

APPLICANT: Harrop, Jeremy A.

APPLICANT: Holmes, Stephen D.

APPLICANT: Reddy, Manjula P.

APPLICANT: Truneh, Aleksej

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION: Receptor-Like 2 (TR2) Antibodies

FILE REFERENCE: GH50027C1

CURRENT APPLICATION NUMBER: US/10/020,787

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 09/403,815

PRIOR FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: PCT/US98/09744

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/046,249

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1704

TYPE: DNA

ORGANISM: Homo sapien

US-10-020-787-1

Query Match 92.7%; Score 547.6; DB 14; Length 1704;
Best Local Similarity 99.3%; Pred. No. 1e-153;
Matches 550; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 60
Db 265 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 324
QY 61 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTCTGTACGCCCGAGCTCTGCCG 120
Db 325 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTCTGTACGCCCGAGCTCTGCCG 384
QY 121 TCTGCAAGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCCAGGT 180
Db 385 TCTGCAAGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCCAGGT 444
QY 181 TATCTGTCAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 240
Db 445 TATCTGTCAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 504
QY 241 GGCACCTACATTTGCCACCTCAATGGCCTTAAGCAAGTGTCTGCAGTGCMAATGTGAC 300
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QY 301 CCAGCCATGGGCTTGGCGGAGCGGACTGCTCCAGGACAGAGAACCGGTGTGGC 360
Db 565 CCAGCCATGGGCTTGGCGGAGCGGACTGCTCCAGGACAGAGAACCGGTGTGGC 624
QY 361 TGAGGCCAGGCGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 420
Db 625 TGAGGCCAGGCGCACTTCTGCACTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 684
QY 421 TAGGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 480

685 TACGCCACTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 744
481 CTGTGTCTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAG 540
745 CTGTGTCTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGAG 804
541 CACCAGACCAATTG 554
805 CACCAGACCAAGTG 818

RESULT 14
3-10-305-720-937
Sequence 937, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
PRIORITY FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 937
LENGTH: 976
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040010136A1 778806
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ... (976)
OTHER INFORMATION: a, t, c, g, or other
3-10-305-720-937

Query Match 57.6%; Score 340.2; DB 16; Length 976;
Best Local Similarity 83.2%; Pred. No. 1.1e-91;
Matches 462; Conservative 0; Mismatches 3; Indels 90; Gaps 3;

1 ATGGAGCTCTGGAGACTGGGGCTCTCCCTGGAGATCCACCCCGACACCGACGTC 60
121 ATGGAGCTCTGGAGACTGGGGCTCTCCCTGGAGATCCACCCCGACACCGACGTC 180
61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCTCTGCTACGCCCCCAGCTCTGCCG 120
181 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCTCTGCTACGCCCCCAGCTCTGCCG 240
121 TCCTGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 180
241 TCCTGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 300
181 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
301 TA---TGTGAGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 357
241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCCTCAATGTGTGAC 300
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301 CCAGCATGGGCTCGCGGAGCGGAACTGCTCCAGGACAGAGAACCGCGTGTGGC 360
418 ----- 417
361 TGCAGCCAGGCCACTTCTGATCGTCCAGGACGGGACCACTGCGCGCGTCCCGCT 420
418 -----CCAGGACGGGACCACTGCGCGCGTCCCGCT 451
421 TACGCCACTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 480

Db 452 TACGCCACTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 511
QY 481 CTGTGTCTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGCA 539
Db 512 CTGTGTCTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTTGGAGGAATGTGCA 571
QY 540 GCACCAGACCAATTG 554
Db 572 GCACCAGACCAAGTG 586

RESULT 15
US-10-369-300-3
Sequence 3, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/358,463
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1082
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (185) .. (1012)
OTHER INFORMATION:
US-10-369-300-3

Query Match 43.9%; Score 259.6; DB 16; Length 1082;
Best Local Similarity 66.8%; Pred. No. 1.4e-67;
Matches 370; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

1 ATGGAGCTCTCTGGAGACTGGGGCTCTCTCTGGAGATCCACCCCGACAAACCGACGTC 60
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61 TTGAGGTGTGTGTATCTACCTTTCTGGAGCCCTCTGCTACGCCCCCAGCTCTGCCG 120
245 TTCAGGTGTGTGTGTGTCTTCTTGAAGTGTGTGAGGGCATCTGTGCCAGCC 304
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGTGCCCAAGTGCAGTCCAGGT 180
305 TCATGCAAGACAGGAGGAGTTCCTTGTGGGAGAGAGTGTGTGCCCAAGTGCACACCAGGT 364
181 TATCGTGTGAAGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
365 TACCATGTGAAGCAGGTCTGAGTGCATACAGGACAGTGTGTGCCCTTCTCCCA 424
241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTGTGCAGTGCCTCAATGTGTGAC 300
425 CAGACATATACCGCCCAATGCAATGGCTTGAAGAGTGTGTGCCCTTGGAGGTCCTGTGAT 484
301 CCAGCATGGGCTCGCGGAGCGGAACTGCTCCAGGACAGAGAACCGCGTGTGTGGC 360
485 CCAGCATGGGCTCGCGGAGCTGCTGCGAGGAGTGTCCAGTGGAGGACACTGTGTGACAG 544
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545 TGCATCCAGGCTACTTCTGTGAGAACCGAGTGGAGCCACTGTTCACATGCTTGCAG 604
421 TACGCCACTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 480
605 CACACCACTTGCCTTCCAGGGCAGAGGGTAGAGAGAGGAGTCTCAGACCGAGGACACT 664

481 CTGTCAGACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTCAG 540
665 GTATGTGCTGACTGGCCTAACAGGGACCTTCTCACTTGGAGGACTCAGGGAATGCCTG 724
541 CACCAGACCAATTG 554
725 CCTGGACCACTG 738

Arch completed: June 10, 2004, 12:07:55
Time: 352 secs

GenCore version 5.1.6
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file: US-09-934-289a-19

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tal number of hits satisfying chosen parameters: 55026578

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Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

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6: em_estpl:*

7: em_estro:*

8: em_hci:*

9: gb_est1:*

10: gb_est2:*

11: gb_hci:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pq:*

27: em_gss_val:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	550.8	93.2	880	12	BI911036	BI911036	603068760
2	550.8	93.2	1012	12	EM912840	EM912840	AGENCOURT
3	550.8	93.2	1200	13	EX436515	EX436515	EX436515
4	550.8	93.2	1612	11	BC018882	BC018882	Homo sapi

5	549.2	92.9	867	12	BI908661	BI908661	603066783
6	549.2	92.9	877	12	BI760906	BI760906	603043783
7	549.2	92.9	884	13	BU528337	BU528337	AGENCOURT
8	549.2	92.9	928	12	BG761765	BG761765	602717963
9	549.2	92.9	973	12	BG761036	BG761036	602717546
10	549.2	92.9	1040	12	BM928475	BM928475	AGENCOURT
11	549.2	92.9	1046	12	BM919433	BM919433	AGENCOURT
12	549.2	92.9	1057	12	BM546990	BM546990	AGENCOURT
13	549.2	92.9	1068	12	BM920057	BM920057	AGENCOURT
14	549.2	92.9	1106	12	EM808047	EM808047	AGENCOURT
15	546.2	92.4	945	13	BQ646947	BQ646947	AGENCOURT
16	542.8	91.8	863	13	BQ228463	BQ228463	AGENCOURT
17	541.4	91.6	1104	13	EX434044	EX434044	60304044
18	540.8	91.5	895	12	BI761634	BI761634	603046357
19	538.2	91.1	779	12	BI518729	BI518729	603061905
20	538.2	91.1	819	12	BG763109	BG763109	602734992
21	538.2	91.1	856	12	EM014603	EM014603	603640415
22	537.2	90.9	948	13	EX365206	EX365206	60365206
23	536.4	90.8	900	12	BI767552	BI767552	603061455
24	534.2	90.4	681	13	EX103478	EX103478	603043478
25	529.6	89.6	942	13	BO719775	BO719775	AGENCOURT
26	528.8	89.5	1005	12	EM919889	EM919889	AGENCOURT
27	528.4	89.4	1201	9	AL513836	AL513836	603088052
28	526.2	89.0	799	12	BI838914	BI838914	603088052
29	526.2	89.0	825	12	BG766381	BG766381	602739122
30	520.8	88.1	1052	12	EM922691	EM922691	AGENCOURT
31	520.2	88.0	1141	13	EX363980	EX363980	60363980
32	517.6	87.6	940	9	AL553857	AL553857	603088052
33	517.6	87.6	1091	12	EM926437	EM926437	AGENCOURT
34	517.4	87.5	1018	12	EM921865	EM921865	AGENCOURT
35	514.6	87.1	1000	10	BF795808	BF795808	602252337
36	513.6	86.9	763	12	BI839134	BI839134	603090581
37	513	86.8	794	14	CB989754	CB989754	AGENCOURT
38	510.4	86.4	863	12	BG766329	BG766329	602739015
39	509.8	86.3	1071	12	EM915482	EM915482	AGENCOURT
40	507.8	85.9	897	12	BI856292	BI856292	603387535
41	506	85.6	850	12	EM009132	EM009132	6036229504
42	485.8	82.2	857	12	BI488633	BI488633	603021165
43	483.2	81.8	816	12	BG765950	BG765950	602738002
44	482.6	81.7	787	12	BI523671	BI523671	603051830
45	482	81.6	754	12	BI752687	BI752687	603021780

ALIGNMENTS

RESULT 1
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LOCUS 603068760Fl NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217830 5',
DEFINITION mRNA sequence.
ACCESSION BI911036
VERSION BI911036.1 GI:16174565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 880)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1547 row: g column: 15
High quality sequence stop: 834.

FEATURES	source	Location/Qualifiers	ORGANISM	SOURCE
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/clone="IMAGE:5217830"		/tissue type="leukocyte"		
/lab_hosts="DH10B"		/clone_lib="NIH_MGC_118"		
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."				
Query Match 93.2%; Score 550.8; DB 12; Length 880;				
Best Local Similarity 99.6%; Pred. No. 1.3e-113;				
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
1 ATGGAGCTCTCGAGACTGGGGCTCTCTCTCGAGATCCACCCCGAGACCGAGTC 60				
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152 TTGAGCTGTGCTGTATCTACCTTCTGGAGCCCTCTAGCGCCCGAGCTCTGCCG 211				
121 TCCTCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTCCAGGT 180				
212 TCCTCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTCCAGGT 271				
181 TATCGTGTGAAGAGGCTGCGGGAGCTGACGGGCACAGTGTGTGAACCTGCGCTCCA 240				
272 TATCGTGTGAAGAGGCTGCGGGAGCTGACGGGCACAGTGTGTGAACCTGCGCTCCA 331				
241 GGCACCTACATTCGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTGTGTGAC 300				
332 GGCACCTACATTCGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTGTGTGAC 391				
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361 TGCAGCCAGGCGCACTTCTGCATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 420				
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421 TACGCCACTCCAGCCCGGCGCAGAGGTGTGCAAGGAGGACCACTGCGCGCGGTGCGCGCT 480				
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481 CTGTGTGAGAACTGCGCGCGGACCTTCTCTCCCAATGGGACCTTGAGGAAATGTGAC 540				
572 CTGTGTGAGAACTGCGCGCGGACCTTCTCTCCCAATGGGACCTTGAGGAAATGTGAC 631				
541 CACCGACCAATTG 554				
632 CACCGACCAATTG 645				
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AGENCY		6708458	NIH_MGC_120	Homo sapiens
5', mRNA sequence.				cdna clone IMAGE:5749604
BM919840				
BM919840.1		GI:19370219		
EST.				

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 36515
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 5-PRIME mRNA sequence.
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 'RCE Homo sapiens (human)
 'RGANISM Homo sapiens

'ERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 'AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 'TITLE 1 (bases 1 to 1200)
 'JOURNAL Full-length cDNA libraries and normalization
 'MENT Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 280.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0CAP002AF11QPI&cluster=280.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0CAP002AF11QPI.
 Location/Qualifiers
 1. .1200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP002YK21"
 /tissue_type="THYMUS"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

'URES
 source

Query Match 93.2%; Score 550.8; DB 13; Length 1200;
 best Local Similarity 99.6%; Pred. No. 1.5e-113;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGGCTC 60
 187 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGACCGGCTC 246

GIN

61 TTGAGCGTGTGTGTATCTCACTTCTGGAGGCCCTGTCTAGCGCCCGAGCTCTGCG 120
 247 TTGAGCGTGTGTGTATCTCACTTCTGGAGGCCCTGTCTAGCGCCCGAGCTCTGCG 306

121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTGCCCAAGTGCAGTCCAGGT 180
 307 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTGCCCAAGTGCAGTCCAGGT 366

181 TATCTGTGTGAGAGGCGCTCGGGGAGCTGACGGGCAACAGTGTGTGAACCTTGCCTCCA 240
 367 TATCTGTGTGAGAGGCGCTCGGGGAGCTGACGGGCAACAGTGTGTGAACCTTGCCTCCA 426

QY 241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 300
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 QY 301 CCAGCCATGGGCGCTGCGCGGAGCGGAACTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 360
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 Db 667 CTGTGTGAGAACTGCCCCCGGGGAGCTTCTCTCCCAATGGGACCCCTGGAGGAATGTTCAG 726
 QY 541 CACCAGACCAATTG 554
 Db 727 CACCAGACCAAGTG 740

RESULT 4
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 LOCUS
 DEFINITION Homo sapiens tumor necrosis factor receptor superfamily, member 14
 (herpesvirus entry mediator), mRNA (cDNA clone IMAGE:3614371).

ACCESSION BC018882
 VERSION BC018882.2 GI:33870063
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 1612)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
 2 (bases 1 to 1612)
 AUTHORS Strausberg, R.

TITLE Direct Submission
 JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:17403015.

COMMENT Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC/DCFT/DTF
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mc@hgrl.nih.gov

AKhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
DiStreich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaapi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IPAL Plate: 12 Row: n Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10835009
This clone has the following problem: no 5' EST match.

FEATURES

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/clone="IMAGE:3614371"
/tissue type="Skin, melanotic melanoma."
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/note="Vector: pOTB7"

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Best Local Similarity 99.6%; Pred. No. 1.7e-113;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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267 ATGAGGCTCTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGACGTC 326
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387 TCCTGCAAGGAGGAGGAGTACCCAGTGGCTCCGAGTGTGCCCCAGTCCAGGT 446
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447 TATCGTGTGAAGGAGGCTGCGGGGAGGTGACGGGACAGTGTGTGAACCTGCCCTCCA 506
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507 GGCACCTACATGCCCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCCTCAATGTGAC 566
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361 TCGACCCAGGCGCACTTCTGATCGTCAGGAAGCGGAGCACTGCGCGCGGTCCCGCT 420
627 TCGACCCAGGCGCACTTCTGATCGTCAGGAAGCGGAGCACTGCGCGCGGTCCCGCT 686
421 TACGCCACTCCAGCCCGGCGCAGAGGTGAGAAAGGAGGACACAGAGTCAAGGACAC 480
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VERSION BI908661.1 GI:16171684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1A011542 Row: e Column: 21
High quality sequence stop: 793.
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/clone="IMAGE:5215868"
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

Query Match 92.9%; Score 549.2; DB 12; Length 867;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGACGTC 60
DB 81 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGACGTC 140
QY 61 TTGAGGCTGTGTATCTACCTTTCTGGAGCCCTCTCTACGCCCGACGTCGCG 120
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DB 201 TCCTGCAAGGAGGAGGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAGTCCAGGT 260
QY 181 TATCGTGTGAAGGAGGCTGCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
DB 261 TATCGTGTGAAGGAGGCTGCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 320
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/organism="Homo sapiens"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

IGIN
Query Match      92.9%; Score 549.2; DB 13; Length 884;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGGAGGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGAACCGACGTC 60
73 ATGGAGGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGAACCGACGTC 132
61 TTGAGGCTGTGTGTATCTACCTTTCTGGAGACCCCTGTGTAGCCGCCAGCTTGCGG 120
133 TTGAGGCTGTGTGTATCTACCTTTCTGGAGACCCCTGTGTAGCCGCCAGCTTGCGG 192
121 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTCCAGTCCAGT 180
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421 TACGCCACCTCCAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
493 TACGCCACCTCCAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTTCCAAATGGGACCTGAGGAGATGTGAG 540
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ORGANISM Homo sapiens
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REFERENCE
1 (bases 1 to 928)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1674 row: m column: 16
High quality sequence stop: 790.
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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FEATURES

source

ORIGIN

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Query Match      92.9%; Score 549.2; DB 12; Length 928;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCGAGAACCGACGTC 60
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Db 194 TTGAGGCTGTGTGTATCTACCTTTCTGGAGACCCCTGTGTAGCCGCCAGCTTGCGG 253
Qy 121 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTCCAGTCCAGT 180
Db 254 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTCCAGTCCAGT 313
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Qy 241 GGCACCTACATTCGACCTCATGCTTAAGCAAGTGTCTGAGTGGCCAAATGTGTGAC 300
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Qy 301 CCAGCCATGGGCTCTGCGGAGCCGGAATGCTCCAGGACAGAGAACCCGCTGTGTGCG 360
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Qy 361 TGCAGCCAGGACCACTTCTGATCTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 494 TGCAGCCAGGACCACTTCTGATCTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 553
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trna sequence.
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BUT 1036
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RGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 973)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1673 row: k column: 12
High quality sequence stop: 779.
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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est Local Similarity 99.5%; Pred. No. 3.2e-113;
atches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCACACCGAGTC 60
114 ATGGAGCTCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCACACCGAGTC 173
61 TTGAGGCTGGTCTGTATCTACCTTTCTGGAGCCCCCTCTACGCCCCAGCTTCGCG 120
174 TTGAGGCTGGTCTGTATCTACCTTTCTGGAGCCCCCTCTACGCCCCAGCTTCGCG 233
121 TCCTCAGAGGAGGAGTACCAGTGGCTCCGAGTCTGCCCGCCAGTCCAGTCCAGGT 180
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ORIGIN

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RESULT 10
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VERSION
BM928475.1 GI:19378854
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1040)
NIH-MGC http://mgc.nci.nih.gov/.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2025 row: 1 column: 10
High quality sequence stop: 626.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5798169"
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/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
FEATURES
source
```

Query Match 92.9%; Score 549.2; DB 12; Length 1040;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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121 TCTGCAAGGAGGACGAGTACCAAGTGGGCTCCAGTGTGTCGCCCCAAGTGCAGTCCAGT 180
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441 TGCAGCCAGGACCACTTCTGATCTGTCAGAGCGGGACCACTTGCCTCCGCGCT 500
421 TACGCCACCTTCAGCCCGGCGAGAGGCTCAGAGGGAGGACCGAGTCCAGGACAC 480
501 TACGCCACCTTCAGCCCGGCGAGAGGCTCAGAGGGAGGACCGAGTCCAGGACAC 560
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561 CTGTGTGAGAACTCCCGCGGAGACCTTCTCTCCAAATGGGACCTTCAGGAAATGTGAC 620
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621 CACAGACCAATTTG 634

SULT 11
919433
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FINITION 6715877 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748693
5', mRNA sequence.

CESSION
RSION
YWORDS
URCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
MMENT

1 (bases 1 to 1046)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM12776 row: n column: 22
High quality sequence stop: 627.

FEATURES
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/clone="IMAGE:5748693"
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source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 Kb, insert size range 1-2.5 Kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 92.9%; Score 549.2; DB 12; Length 1046;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGAGCTCTGTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCHAGAACCGACGTC 60
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QY 61 TTGAGGCTGTGTCTATCTACCTTCTGGAGACCCCTGTCTAGCCGCCACTCTGGCG 120
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QY 121 TCTGCAAGGAGGACGAGTACCAAGTGGGCTCCAGTGTGTCGCCCCAAGTGCAGTCCAGT 180
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QY 421 TACGCCACCTTCAGCCCGGCGAGAGGCTCAGAGGGAGGACCGAGTCCAGGACAC 480
Db 501 TACGCCACCTTCAGCCCGGCGAGAGGCTCAGAGGGAGGACCGAGTCCAGGACAC 560
QY 481 CTGTGTGAGAACTCCCGCGGAGACCTTCTCTCCAAATGGGACCTTCAGGAAATGTGAC 540
Db 561 CTGTGTGAGAACTCCCGCGGAGACCTTCTCTCCAAATGGGACCTTCAGGAAATGTGAC 620
QY 541 CACAGACCAATTTG 554
Db 621 CACAGACCAATTTG 634

RESULT 12
BM546990
LOCUS
DEFINITION
AGENCOURT 6491298 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723783
5', mRNA sequence.
ACCESSION
BM546990
KEYWORDS
BM546990.1 GI:18780404
EST.
SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1057)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L12M12711 row: p column: 24
High quality sequence start: 16
High quality sequence stop: 689.

Location/Qualifiers
1..1057

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5723783"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

3IN

Query Match 92.9%; Score 549.2; DB 12; Length 1057;
est Local Similarity 99.5%; Pred. No. 3.3e-113;
atches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAGCCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGACGACGTC 60
101 ATGAGCCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGACGACGTC 160
61 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTGCTACGCCCGCAGCTCTGCCG 120
161 TTGAGGCTGGTGTATCTCACTTCTGGAGCCCTGCTACGCCCGCAGCTCTGCCG 220
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 180
221 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 280
181 TATCGTGTGAGGAGGCTGGGGAGCTGACGGGACAGTGTGAACCTGCCCTCCA 240
281 TATCGTGTGAGGAGGCTGGGGAGCTGACGGGACAGTGTGAACCTGCCCTCCA 340
241 GGCACCTACATTTGCCACCTCAATGGCCCTTAAGCAAGTGTCTGCAAGTGCACCAATGTGTGAC 300
341 GGCACCTACATTTGCCACCTCAATGGCCCTTAAGCAAGTGTCTGCAAGTGCACCAATGTGTGAC 400
301 CCAGCCATTTGGGCTCGGGCGAGCCGGAATCTGCTCAGGACAGAGAACGCCGTGTGTGAC 360
401 CCAGCCATTTGGGCTCGGGCGAGCCGGAATCTGCTCAGGACAGAGAACGCCGTGTGTGAC 460
361 TGCAGCCAGGACCACTTCTGATCTGCTCAGGACAGGACCACTGCGCGCGGTGTGCCCGCT 420
461 TGCAGCCAGGACCACTTCTGATCTGCTCAGGACAGGACCACTGCGCGCGGTGTGCCCGCT 520
421 TACGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGGGACCGAGAGTCAAGACACC 480
521 TACGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGGGACCGAGAGTCAAGACACC 580

QY 481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTTCCAAATGGGACCTGGAGAAATCTGAG 540
Db 581 CTGTGTGAGAACTGCCCCCGGGGACCTTCTTCCAAATGGGACCTGGAGAAATCTGAG 640
QY 541 CACCAGACCAATTG 554
Db 641 CACCAGACCAATTG 654

RESULT 13
BM920057 1068 bp mRNA linear EST 12-MAR-2002
LOCUS
DEFINITION
AGENCOURT 6706583 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5749919
5', mRNA sequence.

ACCESSION
BM920057
VERSION
BM920057.1 GI:19370436
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1068)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L12M12780 row: a column: 24
High quality sequence stop: 674.

Location/Qualifiers
1..1068

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5749919"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 92.9%; Score 549.2; DB 12; Length 1068;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGACGACGTC 60
Db 97 ATGAGGCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGACGACGTC 156
61 TTGAGGCTGTGTGTATCTCACTTCTGGAGCCCTCTGCTACGCCCGCAGCTCTGCCG 120
157 TTGAGGCTGTGTGTATCTCACTTCTGGAGCCCTCTGCTACGCCCGCAGCTCTGCCG 216
QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 180
Db 217 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 276
QY 181 TATCGTGTGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240

277 TATCGTGTGAAGAGGCTCGCGGAGCTGACGGCAGTGTGTGAACCTCGCTCCCA 336
241 GGCACCTTACATTCCTCCACCTCAATAGCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGAC 300
337 GGCACCTTACATTCCTCCACCTCAATAGCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGAC 396
301 CCAGCCATGGGCTCGCGGAGCGGAACTCTCCAGAGCAGAGAGCGCGTGTGCG 360
397 CCAGCCATGGGCTCGCGGAGCGGAACTCTCCAGAGCAGAGAGCGCGTGTGCG 456
361 TGCAGCCAGGCTTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGT 420
457 TGCAGCCAGGCTTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGT 516
421 TAGCCACCTTCAGCGCGGCGGAGGCTGCAAGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGG 480
517 TAGCCACCTTCAGCGCGGCGGAGGCTGCAAGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGG 576
481 CTGTGTGCAAGTGTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGG 540
577 CTGTGTGCAAGTGTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGG 636
541 CACAGACCAATTG 554
637 CACAGACCAATTG 650

RESULT 14
4806047
XUS
DEFINITION BM806047 1106 bp mRNA linear EST 05-MAR-2002
AGENCOURT 6513372 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5731803
5', mRNA sequence.
BM806047
EST.
SYNOPSIS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1106)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12732 row: 0 column: 04
High quality sequence start: 3
High quality sequence stop: 630.
Location/Qualifiers
1. 1106
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/tissue_type="hippocampus"
/lab_host="DR108"
/clone_lib="NIH_MGC_124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: EcorV
(destroyed); Site: 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN
Query Match 92.9%; Score 549.2; DB 12; Length 1106;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAGGCTCTCGAGCTGGGGGCTCTCTCTCGAGATCCACCCCGAGACGAGTC 60
DB 80 ATGAGGCTCTCGAGCTGGGGGCTCTCTCTCGAGATCCACCCCGAGACGAGTC 139
QY 61 TTGAGGCTGTGTATCTACCTTTCTGGAGGCGGCTCTACGCCCCAGCTTGTGCG 120
DB 140 TTGAGGCTGTGTATCTACCTTTCTGGAGGCGGCTCTACGCCCCAGCTTGTGCG 199
QY 121 TCTGCAAGGAGGAGGAGTACCCAGTGGGCTCCAGTGTGCTGCCCAAGTGCAGTCCAGT 180
DB 200 TCTGCAAGGAGGAGGAGTACCCAGTGGGCTCCAGTGTGCTGCCCAAGTGCAGTCCAGT 259
QY 181 TATCTGTGAAGAGGAGGCTCTCGGAGCTGACGGGCAAGTGTGAAACCTGCTCCA 240
DB 260 TATCTGTGAAGAGGAGGCTCTCGGAGCTGACGGGCAAGTGTGAAACCTGCTCCA 319
QY 241 GGCACCTTACATTCCTCCACCTCAATAGCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGAC 300
DB 320 GGCACCTTACATTCCTCCACCTCAATAGCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGAC 379
QY 301 CCAGCCATGGGCTCGCGGAGCGGAACTCTCCAGAGCAGAGAGCGCGTGTGCG 360
DB 380 CCAGCCATGGGCTCGCGGAGCGGAACTCTCCAGAGCAGAGAGCGCGTGTGCG 439
QY 361 TGCAGCCAGGCTTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGCT 420
DB 440 TGCAGCCAGGCTTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGCT 499
QY 421 TACGCCACCTTCCAGCGGCGGAGGCTGCAAGAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGG 480
DB 500 TACGCCACCTTCCAGCGGCGGAGGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 559
QY 481 CTGTGTGCAAGTGTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGT 540
DB 560 CTGTGTGCAAGTGTCTGCAATTCCTGCAAGCAGGAGCGGAACTCTCCAGAGCAGAGAGCGCGT 619
QY 541 CACAGACCAATTG 554
DB 620 CACAGACCAATTG 633
RESULT 15
BQ646947
LOCUS
DEFINITION BQ646947 945 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8302463 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271311
5', mRNA sequence.
BQ646947
VERSION BQ646947.1 GI:21771119
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 945)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Ruben Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M2447 row: n column: 16

High quality sequence start: 8
High quality sequence stop: 627.
Location/Qualifiers
1. .945
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6271311"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_100"
/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

IGIN

Query Match 92.4%; Score 546.2; DB 13; Length 945;
Best Local Similarity 99.5%; Pred. No. 1.5e-112;
Matches 548; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
4 GAGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAAGCGAGCTCTTG 63
|||
21 GAGGCTCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAAGCGAGCTCTTG 80
|||
64 AGGCTGGTCTCTACTCTACCTTCTGGAGCCCTCTAGCCGCCAGCTCTCCGCTCC 123
|||
81 AGGCTGGTCTCTACTCTACCTTCTGGAGCCCTCTAGCCGCCAGCTCTCCGCTCC 140
|||
124 TGCAAGGAGGAGGATACCCAGTGGGCTCCGAGTCTGCCCAAGTGCAGTCCAGGTTAT 183
|||
141 TGCAAGGAGGAGGATACCCAGTGGGCTCCGAGTCTGCCCAAGTGCAGTCCAGGTTAT 200
|||
184 CGTGTGAAGGAGGCTGGGGAGCTGACGGGCAAGTGTGTGAACCTTGCCTCCAGGC 243
|||
201 CGTGTGAAGGAGGCTGGGGAGCTGACGGGCAAGTGTGTGAACCTTGCCTCCAGGC 260
|||
244 ACTACATTCGCCCACTCAATGGCTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGACCCA 303
|||
261 ACTACATTCGCCCACTCAATGGCTAAGCAAGTGTCTGCAGTGCCTAAATGTGTGACCCA 320
|||
304 GCCATGGGCTTCGGCGGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGC 363
|||
321 GCCATGGGCTTCGGCGGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGC 380
|||
364 AGCCAGGCGCACTTCTGCATCTCCAGGACGGGACCACTGCGCGCGTGCCTGCTTAC 423
|||
381 AGCCAGGCGCACTTCTGCATCTCCAGGACGGGACCACTGCGCGCGTGCCTGCTTAC 440
|||
424 GCCACCTTCAGCCCGGCGCAGAGGTGCAGAGGAGGACCCGAGAGTCAAGACACCTTG 483
|||
441 GCCACCTTCAGCCCGGCGCAGAGGTGCAGAGGAGGACCCGAGAGTCAAGACACCTTG 500
|||
484 TGTCAAGACTGCCCCCGGGGACCTTCTCTCCATGGGACCTTGGAGGATGTACACAC 543
|||
501 TGTCAAGACTGCCCCCGGGGACCTTCTCTCCATGGGACCTTGGAGGATGTACACAC 560
|||
544 CAGACCAATTG 554
|||
561 CAGACCAAGTG 571
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Arch completed: June 10, 2004, 11:04:41
Time: 2516 secs